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AG121669 pan trog1
AA781423 a126C03.s
AW9711553 EST383642
AG033781 pan trog1
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AQ082947 HS_3131_B
A112856 qc61h10.x
AI393478 tg45590.x
AG036829 pan trog1
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BI087886.1 GI:
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Hammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 771)
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    225
    ø
                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4993894"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.5 kb. Library prepared by Life
Technologies."
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Pan troglodytes DNA, clone: PTB-130M15.F

AGI21669

AGI21669.1 GI:16650834

GSS; GSS (genome survey sequence).

Pan troglodytes male lymphoblast DNA, cl

BAC Library clone:PTB-130M15.F.

Pan troglodytes

Pan troglodytes
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        BAC end sequences of Libr
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2 (bases 1 to 689)
Fujiyama,A., Hattori,M.,
Totoki,Y., Watanabe,H. an
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570; Conser
                                                        Fujlyama,A., Hattori,M., To
Totoki,Y., Watanabe,H. and
                                                                                                Eukaryota; Metazoa;
                                                                                       Mammalia; Eutheria;
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Pred. No. 7.7e-93;
0; Mismatches 49
          and
          Toyoda,A., Taylor,T.D., nd Sakaki,Y.
                                                         Toyoda, A.,
nd Sakaki, Y.
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                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
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CCACCAATGGCTACCCTCTTTGGGTCCCCTCCCTTTGTTATGG
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                                                                      TTATTGCCTGAGAGTACAGCGGGAAGGACAATGATCGGGGATATAAACTCATGCATTCGAG
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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/clone_lib="PTB Chimpanzee Male
/clone_lib="PTB Thimpanzee Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-130M15.F"
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D; Mismatches 58;
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                                                                                                                                                                                                                                                                                                               Local
ctgcacaacccctactatgccccaattcagcgggaagcagttagagcggtcatcagccaa 250
                                                                                                                                cctccccaacagcacttgggttttcctgttgagaggggggactgaggagacaggactagct 310
                                                           GGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACCACATCCACCT
                                                                        ggatttcctaggccaacgaagaatccctaagcctagctgggaaggtgactgcatccacct 370
                                                                                                                 CCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAGACAGGACTAGCT
                                                                                                                                                                           CTGCACAACCTCTACGCCCCCAATTCAGCAGGAAGCAGTTAGAGCGGTCGTCGGCCAA 375
                                                                                                                                                                                                                                    CTGCTAGCCCACGATCTGATGTTAATGACATCAAAGGCACCCCTCCTGAGGAAATCTCAG 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1645 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 475.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 494)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: M. Bento Soares, Ph.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="1391428"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_testis_NHT"
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92.7%;
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Primates;
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Pred. No. 1.6e-82;
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The Institute for Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: johnq@tigr.org
Plate: 292
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91.8%;
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522 AGGTTTAAGATCTTCCGCGGACCCCTAAAACTGGCTTGCTAGCCCCATGTTCTGGTGTTAA 463
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                                                                         GTTCAGCAGGAAGCAGTTAGAGTGGTCATCAGCCAACCTCACCAACAGCACTTGGGTTTT 343
                                                                                                                                               TGACATCGAAGTCACTCCTCCTGAGGAAATTCTCAACTGCACAACCCTTATTATGCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Dr., Rockville, Tel: 301 838 3528
Fax: 301 838 0208
Fmail: 4ch-ch:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quackenbush, J.
Assessment of gene expression patterns in a model metastasis using a 19,200 element cDNA microarray
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EST383642 MAGE resequences, MAGL Homo sapiens
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Hegde, P., Qi, R., Abernathy, K., Dharap, S.,
, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Y.
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_oref="MAGE resequences, |
/clone_lib="MAGE resequences, |
/note="Vector: pBluescriptSKm"
115 c 134 g 148 t
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Pred. No. 1.5e-81
D; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan troglodytes DNA, clone: PTB-008021.F, genomic survey sequer AG033781 AG033781.1 GI:16560654 GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee BAC Library clone:PTB-008021.F.
                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama, A., Hattori, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
             Similarity
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R.Site 1 : SacI
R.Site 2 : SacI.
Conservative
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/db_xref="taxon:9598"
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/cell_type="1ymphoblast"
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88.0%;
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            Score 423; DB 12; Pred. No. 1.3e-79;
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nd Sakaki, Y.
Mismatches
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2 others
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                                                                                                                                                                                             (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                           tn14a10.x1
similar to
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                           Bonaldo,
                                                                                                                                                            Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Insert Length:
                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                            cgapbs-r@mail.nih.gov
                                                                                                           Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         490 bp mRNA linear EST 12-MAY-1999 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167578 3' contains PTR5.tl PTR5 repetitive element;, mRNA
                                                                                                                                                            M.D., Myrna R.
                                                                        Sequencing Center
                                                          information
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                                                                                                                                                                                                                                                                           CACCTTTAAACACGGGGCTTGCAACTTAGCTCACACCCGACCAATCAGAGGGCTCACTAA
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Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 440)
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601571305F1 NIH_MGC_21 Homo s
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                                                                                mRNA sequence.
                                        human.
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35; Conservative
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/clone_lib="NCI_CGAP_Brn25"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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92.9%;
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                                                 CTATTAAATCTTGCAACTG
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GTCGTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGATGGGGGACTGAGAG 120
                                                                                                         ACAGGACTAGCTGGATTTCCTAGGCTGACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGA
                        ctattaaatcttgcaactg 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes
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/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note="organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.

Site_2: EcoRI; cDNA made by oligo-dT priming.

Birectionally cloned into EcoRI/XhoI sites using the placent size 1.8kb. Library constructed by for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

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/clone_lib="NIH_MGC_21"
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/db_xref="taxon:9606"
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Pred. No. 3.9e-74;
0; Mismatches 26;
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Matches 467
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483
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Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
                                                                                                       ctagcccatgctccgatgttaatgacattgaaaggcacccctcccgaggaaatctccaactg 193
                                                                                   CTAGCCCA-GCTCCCACATTAATGACATCAAAGGCACCCCTCCCGAGGAAATCTCAACTG
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467; Conserv
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B1963185
B1963185.1 GI:16337590
EST.
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Library was constructed by Dr. Douglas Melton DNA sequencing by
Washington University Genome Sequencing Center For information
Obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 617-495-1812
Fax: 617-495-8557
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Honaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
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123 c 147 g 156 t 1 others
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Islets of Langerhans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Both"
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                                                                                                                                                                                                                                                                             62.4%;
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Pred. No. 7.2e-74;
0; Mismatches 51;
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Vokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, UKL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the Chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes DNA, clone: PTB-046A08 AG058970
AG058970.1 GI:16596431
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, BAC Library clone: PTB-046A08.R.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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R.Site
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                                                                                                                                                                                                                                                                                                                                                                                  tracking errors.
                                                             /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
160 c 159 g 191 t
                                                                                                                                                                 /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                 1. .651
                                                                                                                           /sex-"male"
                                                                                                                                               /clone-"PTB-046A08
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Sutheria; Primates; Catarrhini; Hominidae;
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RESULT 10
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                                                                                                                                                                                                                                                                           AG126669 701
Pan troglodytes DNA, clone: P
AG126669
AG126669.1 GI:16655834
GSS: GSS (genome survey seque
Pan troglodytes male lymphobbl
BAC Library clone:PTB-137E19.
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC ence was generated during the R&D process and may have higher chance of
                                                                                                                                                                                       Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                  Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                     Direct Submission
                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                      (sites)
                                                                                                                                             (bases 1 to 701)
                                                                                                                                                                             end
                                                                                                                                                                                                                                                                            ; GSS (genome survey sequence). troglodytes male lymphoblast DNA, Library clone:PTB-137E19.F.
                                                                                                                                                                                                                                                                troglodytes
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                                                                                                                                                                             sequences
                                                                                                                                                                                                                                                 Metazoa;
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                                                                                                                                                                             of Library
                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 394.8; DB 1
Pred. No. 1.2e-73;
0; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                              701
                                                                                                                                                                                                                                                                                                                                                  1 bp DNA
PTB-137E19.F,
                                                                                                                                Taylor, T.D., Yada, T.
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                                                                                                                                                                                                       Taylor, T.D.,
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                                                                                                                                                                                                                                                                                           clone_lib:PTB Chimpanzee
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genomic
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Mammalia; Eutheria;
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CCATGCTGCAATGTTAATGACATTGAAGGCACCCCTGCCCGAGGAAATCTCAACTGCACA
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Pan troglodytes DNA, clone: PTB-056L1s
AG06690.1 GI:16618703
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone: PTB-056L15.F.
Pan troglodytes
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R.Site 2
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
/clone_lib="182 g 195 t
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1. No. 2.6e-73;
1. No. 53;
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                                  clone_lib:PTB
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Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae.

Euteleostomi;

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              acccaggcattcgagccggcaacggcaacccctttgggtccccttccctttgtatgggcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-7-22 Suchito-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suchito-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end Clones are derived from the chimpanzee BAC library PTB This BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiyama, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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R.Site 2 : SacI.
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/clone_lib="PTB Chimpanzee Male BAC Library"
141 c 165 g 176 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pan troglodytes'
/db_xref="taxon:9598"
/clone="PTB-056L15.F"
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87.7%;
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Pred. No. 3e-73;
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nd Sakaki,Y.
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome

Clone distribution: NCI-CCAP clone distribution

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1375 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., I
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
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National Cancer Institute, Cancer Genome Ana
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1 (bases 1 to 443)
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/db_xref="taxon:9606"
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                                                                                                                                                     Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 313 row: J column: 8
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seati Tel: (206) 616-3618 Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                          scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17),
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Mammalia; Eutheria;
1 (bases 1 to 712)
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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             161
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Location/Qualifiers
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                                                             /organism="Homo sapiens"
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/clone="plate=3131 Col=8 Row=J"
/clone_lib="CIT Approved Human Genomic Sperm Library
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                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
Insert Length: 720 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
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Mammalia; Eutheria;
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                                             High quality sequence stop: 428 Location/Qualifiers
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National Cancer Institute, Cancer Genome Ana
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Tumor Gene Index
Unpublished (1997)
Contact: Robert St
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 446).

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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/db_xref="taxon:9606"
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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                                                             ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 876-5891
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Merberg, David
APPLICANT: Mreberg, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PF
TITLE OF INVENTION: ENCODING TI
                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MOLECULE TYPE:
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CITY: C
                              STRANDEDNESS:
                                                                                                                                                                                                                         CLASSIFICATION: 536
                TOPOLOGY:
                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/686,878A
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5. 5708157
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                                                nucleic acid
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Lavallie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics Institute,
                              double
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US-08-721-489-4
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Best Local Similarity
Matches 245; Conserv
                                                                                              TELEFAX: (617) 876-58
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/721,489
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                               REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 5
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                                                                               SEQUENCE CHARACTERISTICS:
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                              LENGTH: 279 LL
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                             STRANDEDNESS: double
                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 87 Cambi
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               TOPOLOGY:
                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                           87 CambridgePark Drive
                                                            279 base pairs
                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
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LaVallie, Edward
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                 linear
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                                                                                           7) 450
) 876-5851
- NO: 4:
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88.1%;
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Pred. No. 7.6e-66;
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US-08-691-563C-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46, Application
                                                                                                                           FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: BETTIAGE, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                TELEFAX: 703-836-2/8/
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACTITLE OF INVENTION: THERAPEUTIC PURPOSES
                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Colette JOLIVET
APPLICANT: Bernard MANDRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: Alexandria
STATE: Virginia
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                                                                        1859 base pairs
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88.1%;
                                                                                                                                                                                                                                                               Release #1.0, Version #1.30
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                                                                                                                                                               WPB 38588
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Pred. No. 7.6e-66;
                                                                                                                                                                                                                                                                                                                                                                                               Street, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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gaaatctcaactgcacaacccctactatgccccaattcagcgggaagcagttagagcggt 240

59058

59007

gacactaccactgcagggccccttcttcaccccctatccagcaggaagtagctacagcggt 59118

59008

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; LENGTH: 80246
; TYPE: DNA
; ORGANISM: Nucleotide sequence of NC-contig
US-09-078-294-4
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                                                                                                                Query Match 19.8
Best Local Similarity 67.2
Matches 213; Conservative
                                                                                                                                                                                                                                                                            SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
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                                                                1 ccctgtatctttaacctccttgttaagtttgtctcttccagaatcaaaactgtaaaacta
caaattgttcttcaaatggagcaccagatggagtccatgactaagatccaccgtggaccc 120
                                                cctgtatttttaacctcttggtcaaatttgtttcctctaggatcgaggccatcaagcta
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FOR DIAGNOSTIC,

PROPHYL

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Patent No. 6001900:

GENERAL INFORMATION:

APPLICANT: Herve PERRON

APPLICANT: Frederic BESEME

APPLICANT: Frederic BEDIN

APPLICANT: Glaucia PARANHOS-BACCALA

APPLICANT: Glaucia PARANHOS-BACCALA

APPLICANT: Torence KOMURIAN-PRADEL

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; Patent No. 626521
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Best Local S
Matches 213
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APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
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CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
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nes 213; Conservative
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T: Bernard MANDRAND
INVENTION: VIRAL M
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    VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
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les 92;
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US-08-232-463-14/c
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                                                                                                                                                         Sequence 14, Application US/08232463 Patent No. 5670367
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Best Local :
                                                 GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 703-836-2787 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PATENTIA RELEASE #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/691 <----
FILING DATE: 05.000
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ATTORNEY/AGENT INFORMATION:
NAME: BETTIDGE, William P.
REGISTRATION NUMBER: 30,024
                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                  ADDRESSEE:
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Pred. No. 2e-30;
0; Mismatches
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COUNTRY:

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US-08-011-398B-1/c
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                                                                                                           Sequence 1, Application US/08011398B Patent No. 5512473
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
             GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7218 base pairs
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CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                         1142
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ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             1082 RRRRRRRRRRRRRRRATCGCAAGCTCCCTCG
                                                                                                                                                                                                                                                                                                                                         1202
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 899149
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54; Mismatches
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                Sequence 1, Application Patent No. 5780262
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOTTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/464,051
FILING DATE: 05 JUN 1995
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                 APPLICANT: Roger Bren APPLICANT: Antonis S.
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TELLEFAX: 200154
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                                                                                                                                                                          ADDRESSEE: Fish -
                                                                                                                             COUNTRY: U.S.A. ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 225 | CITY: Boston
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                                                                                                                                                                                                                                                                                                 Roger Brent
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5 Franklin Street
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Pred. No. 1;
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US-08-462-498-1/c
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Matches
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO: 1:
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REFERENCE/DOCKET NUMBER: 007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
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PRIOR APPLICATION UMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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APPLICANT: VANTONIS S. ZETVOS
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
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LENGTH: 2417
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                                                                                                          NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                    TELEFAX:
                                                                                                                                                                                                                                            CLASSIFICATION: 435
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                                                    (617) 542-8906
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Pred. No.
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Best Local (
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                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PS/2 model 502 or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOPTWARE: Wordperfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTE
TITLE OF INVENTION: MOLECULES AND METHODS
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                        539 ggcaacccctttgggtcccctccctttgtatgggcgctctgttttcactctatttcact 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 TAACTACCCTTAATTACTTAAAAAAAAAAAAAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       539 ggcaaccccctttgggtccccttccctttgtatgggcgctctgttttcactctatttcact 598
                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                           LENGTH: 2417
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: No. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: n
                                                                                                                                                                                                                                                                                                             NAME: Karen F. Lech
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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GGGAAGGCCTCTTGGAGACCTTACCCCTGGCTGTTTGGACTTTGTATACTTTAAATAATT 103
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3. 6017692
                                                         1 Similarity
57; Conserv
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                                                          Conservative
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MAX-INTERACTING PROTEINS AND RELATED
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                                                       O; Mismatches
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Pred. No.
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                                                                                         Sequence 1, Application US/08011398B Patent No. 5512473 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 42, Application US/09247155A Patent No. 6312922
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: sig_peptide
LOCATION: 39. 83
OTHER INFORMATION: Von Heljne matrix
OTHER INFORMATION: score 4.6
OTHER INFORMATION: seq LLTHNLLSSHVRG/VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: polyA_site
LOCATION: 583..598
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NAME/KEY: CDS
LOCATION: 39..413
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             APPLICANT: Roger Brent
APPLICANT: Antonis S.
TITLE OF INVENTION: MA
                                                                                                                                                                                                                                                                                                                                      546
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                                                                                                                                                                                                                       572 ggtttaaaaccaaaaaaaaaaaaaaa 598
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OF,
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                                                                     Roger Brent
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                             3. Zervos
MAX-INTERACTING PROTEINS AND RELATED
MOLECULES AND METHODS 20
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                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08464051 Patent No. 5780262
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Best Local Similarity
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                                                                                                                                                                                                                                                                                      GENERAL
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                          APPLICANT: ROGET BREI
APPLICANT: ARTORIS S
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.1)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               2365
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ADDRESSEE: Fish & Richardson
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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PRIOR APPLICATION DATA:
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              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Paul T. Clark
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
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                                                                                                                                   STATE:
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                                                                                                                   COUNTRY:
                                                                                                                                               CITY: Boston
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APPLICATION NUMBER:
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US/08/464,051
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Pred. No. 3.4;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2417
ILENGTH: 0416
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
-08-464-051-1
                                                                                                                                                                                                                                   Query Match 4.9%; Score 31.4; DB 1; Length 2417; Best Local Similarity 54.9%; Pred. No. 3.4; Matches 62; Conservative 0; Mismatches 51; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 05 JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/011,398
FILING DATE: 29 JAN 1993
ATTORNEY/AGENT INFORMATION:
NAME: PAUI T. CLAE'K
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/160002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPHONE: (617) 542-8906
TELEPA: 200154
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Result
No.
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Perfect score:
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Maximum DB seq length: 2000000000
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  635
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1: /SIDS1/gcgdata/gc
2: /SIDS1/gcgdata/gc
3: /SIDS1/gcgdata/gc
4: /SIDS1/gcgdata/gc
5: /SIDS1/gcgdata/gc
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Match
  100.0
100.0
97.2
85.8
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SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:

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SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:

SIDSI/gcgdata/geneseq/geneseqn-embl/NA2000.BAT:

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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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2460.040 Million cell updates/sec
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Clone CL6-3' from
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Human endogenous

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-Reynaud C, Komurian-Pradel a G, Perron H;						alifiers Encodes protein AAW71067"	d retrovirus.	d retrovirus; MSRV; MS; id arthritis-associated	d retrovirus fragment 4.			BP.	ALIGNMENTS	AA163/61	AA199411	AAS72721	AAS92500	AAS31002	AAS92680	AAH46211 AAS63154	AAS76196	AAH17481 AAS88391	AAS68626	AAS84209 AAS77313	AAS76474	AAS71727 AAS67609	AAS31000	AAA59213 ABA08902	AAX25663	AAI35980 AAI04422	AAI14608	AAK04516	ABA25978	ABA45822	AAA59215	AAH20069	AAA59211	AAA59210 AAX25661
del F;								pol gene; virus; ss.						Human Kidney relat	Human excretory re	DNA encoding novel	DNA encoding novel	Human diagnostic a	DNA encoding novel	Human purified sec	DNA encoding novel	Human cDNA sequenc	DNA encoding novel	DNA encoding novel	DNA encoding novel	DNA encoding novel	Human diagnostic a	pol gene	Human endogenous r	Probe #4666 used t	Probe #4541 for ge	orain expre	Probe #4444 for ge	n breast cell	endogenous	envelope	coding, 3'	3' pol gene and 3' Human endogenous r

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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                                                  caaccccctttgggtcccctccctttgtatgggcgctctgttttcactctatttcactct
                                                                                                               agagcacagcgggagggacaaggatcgggatataaaacccaggcattcgagccggcaacgg
                                                                                                                                                              actaaaatgctaattaggcaaaaatagggaggtaaagaaatagccaatcatctattgcctg
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DB; AAW71067.
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       attaaatcttgcaactgaaaaaaaaaaaaaaaaa
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Best Local Similarity 100.
Matches 635; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid sequences of retrovirus called MSRV-1 multiple sclerosis or rheumatoid polyarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUL-1997;
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   421
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actaaaatgctaattaggcaaaaataggaggtaaagaaatagccaatcatctattgcctg
                                                                                                               aggactagctggatttcctaggccaacgaagaatccctaagcctagctgggaaggtgact
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                                                gcatccacctctaaacatggggcttgcaacttagctcacacccgaccaatcagagagctc
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Pred. No. 2.2e-187;
Mismatches 0;
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The present sequence represents the nucleotide sequence corresponding to the 3' env region and long terminal repeat sequences from clone CL6 of Multiple Sclerosis retrovirus (NSRV-1). The specification describes a long terminal repeat (LTR)-RU5 region which encodes the expression of a MSRV-1 protein. This is unusual for LTRs, in particular in the RU5 region. The sequence includes CAAT and TATA
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s (MSRV) used
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Multiple sclerosis

associated

retrovirus

rheumatoid

arthritis-associated

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a multiple sclerosis (MS) associated retrovirus (MSRV) genomic fragment used in the method of the invention. The invention provides complete or partial genomic sequences of the MSRV-1 pol gene, gag gene and env gene, and polypeptides encoded by these genes. The invention also provides antibodies raised against the polypeptides. The genomic sequences, polypeptides and antibodies are also claimed useful for diagnosing infection by MS and rheumatoid arthritis-associated viruses, and also for prevention and treatment of infection with these viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid from retroviruses - useful prevention and treatment of, e.g. multiple
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stop codon)
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stop codon)
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/transl_except=
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92.4%;
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xcept= (pos:77-79, appears
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 545; DB Pred. No. 3.3e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (pos:125-127,
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3.3e-159;
47;
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Matches 572
                                                                                                 related virus type 1 (MSRVI). The sequence can be used in diagnostic, prophylactic or therapeutic compositions to inhibit expression of a multiple sclerosis related virus and/or virus associated with rheumatoid polyarthritis.
                                                                                 Sequence
                                                                                                                                       This
                                                                                                                                                                         Nucleic acid sequences of retrovirus called MSRV-1 - multiple sclerosis or rheumatoid polyarthritis
                                                                                                                                                                                                                                                                                                                       Multiple sclerosis related virus
                                                                                                                                                                                                                                                                                                                                        Multiple sclerosis; virus; diagnosis; prophylaxis; therapy; expression; rheumatoid polyarthritis; ss.
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Pred. No. 3.3e-159;
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RESULT AAX77526 ID AAX77526 ID AAX77526 ID AAX77 XX AAX7 XX Secr KW bone KW cell KW haen KW cadl XX Home CAY WO95 XX WO95 XX PD 03-1 PF 17-1 PR 20-1 P
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21-NOV-1997;
18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibin; chemotactic; chemothatic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.
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97US-0976110.
98US-0080478.
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Query Match Best Local S Matches 581

Local Similarity nes 581; Conserv

84.18; nilarity 91.58; Conservative

pred. No. 1.5e 0; Mismatches

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Sequence

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polynucleotides isolated from human secreted proteins encoded by CC blood or adult placenta, or murine adult testes, adult brain, adult CC libraries. The products of the invention are predicted to have biological activities which would make them suitable for treating, preventing or CC supporting data is given. Suggested activities include nutritional CC activity, cytokine and cell proliferation/differentiation activity, cytokine succines) or suppressing activity, cytokine and cell proliferation/differentiation activity, CC immune stimulating (e.g. as vaccines) or suppressing activity, haemostatic activity inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, and tumour CC activity, cadherin/tumour invasion suppressor activity, and tumour CC inhibition activity. The polynucleotides are also stated to be useful to
WPI; 1999-357813/30
P-PSDB; AAY08622.
                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                            Page 100-101;
                                                                                                                                                                                                                                                                                                                                                                                                                 encoding secreted
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                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                             Matches 581;
                                                                                                                                                                                                                                                                                                                                                                                                   treating, preventing or ameliorating medical conditions in humans and animals. Detection of the levels of the proteins can be used for the diagnosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemokinetic activity, haematoratic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cablerin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotide sequences are also stated to be useful for gene therapy.
                                                                                            2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the human secreted protein AJ172_2 nucleotide sequence, obtained from a human adult testes cDNA library. The invention relates to secreted human and murine proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; disease diagnosis; pre-eclampsia; cancer placental pathology; metastasis inhibition; nutritional activity; immune stimulator; haematopoiesis regulator; tissue growth; tumour inhibitor; anti-inflammatory; clone AJI72_2; ATCC_98115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; Page 107-108; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                       Sequence
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20-OCT-1998;
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caaattgttcttcaaatggagcaccagatggagtccatgactaagatccaccgtggaccc
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DB; AAY67313.
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Pred. No. 1.5e-155;
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                                                                                                                                                                                                                                   Human endogenous retrovirus
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syncytia; cancer;
                                                                                                                                                                                                                                                                                         Nucleotide sequence of a human endogenous retrovirus envelope protein.
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ilarity 91.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multiple sclerosis; rheumatoid polyarthritis; insulin-dependent disseminated lupus erythematosus; pregnancy; chromosomal marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy
                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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                                             gaaatctcagctgcacaacctctactacgccccaattcagcaggaagcagttagagcggt
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cgtcggccaacctccccaacagcacttaggttttcctgttgagatgggggactgagagac
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Pred. No. 2.9e-153;
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                                                      The present sequence represents an endogenetic retroviral nucleic acid fragment, which is associated with an autoLimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoImmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoImmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid from human endogenous retrovirus, useful e.g. diagnosis of autoimmune disease and complications of pregnancy contains at least part of the gag gene .
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pregnancy; multiple sclerosis; T cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                      Page 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents clone cl.PH74 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin-
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          agagcacagcgggagggacaaggatcgggatataaaccccaggcattcgagccggcaaccgg
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                                                                                                                                                                                                                                                                                   The present sequence represents an endogenetic retroviral nucleic acid fragment, which is associated with an autoLimnune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for dispnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis of autoimmune contains at least part c
                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid from human endogenous retrovirus, useful e.g. diagnosis of autoimmune disease and complications of pregnancy, contains at least part of the gag gene -
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                                                                                                                                                                                                                                                                                                                                                                                                                 endogenous retrovirus; HERV-W; HERV; chromosome 7; env protein; 
ppe protein; multiple sclerosis-related superantigen; vaccine; 
ce antigen; transmembrane; multiple sclerosis; neuroprotective; 
ense-therapy; autoimmune disorder; ds.
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(pos:790.792,aa:Phe)

(pos:793.795,aa:Thr)

(pos:812.814,aa:Leu)

(pos:818.820,aa:Ser)

(pos:865.867,aa:Gln)

(pos:8174.1176,aa:Arg)

(pos:1174.1176,aa:Arg)

(pos:2017.2019,aa:Lys)

(pos:2017.2019,aa:Arg)

(pos:2044.2046,aa:Arg)

(pos:2089.2091,aa:Arg)

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Sequence

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CC designated HERV-W. The present invention describes proteins or peptides (I) having superantique (SA9) activity comprising the ENV protein (ENV) CC of HERV-W, the surface protein (SU) and transmembrane (TM) sub-units. (I) CC have neuroprotective activity, and can be used in: vaccines; antisense-CC useful for diagnosing multiple sclerosis (MS) or HERV-W-associated CC disorders. (I) are also useful for identifying substances (and optionally CC with MS, substances capable of blocking to a retroviral superantigen associated CC capable of blocking transcription or translation of HERV-W retroviral SQG activity and substances (CC devoid of SA9 activity and being capable of blocking transcription or translation of HERV-W retroviral SQG capable of blocking SQG substances (I), modified to be CC devoid of SA9 activity and being capable of generating an immune response CC against HERV-W retroviral SQG is useful in therapy. Nucleic acid CC molecules encoding (I) are useful as vaccines against MS. Substances CC capable of blocking SA9 activity, capable of binding to a retroviral CC superantigen associated with MS, or capable of binding to a retroviral CC capable of blocking SA9 activity, capable of binding to a retroviral custing (I) are useful for the treatment and CC prevention of MS. (I) and nucleic acids encoding them are useful for CC diagnosing autoimmune disease. The present sequence encodes the CC specifically claimed envelope protein of HERV-W designated G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On the basis of the PBS t-RNA motif used for the classification endogenous retrovirus (HERVs) the full length endogenous proviruwas been located on the long arm of human chromosome 7 (7q21-22)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human retrovirus HERV-W ENV proteins/peptides having superantigen activity useful for diagnosing and treating multiple sclerosis -
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                                                                                                                This sequence represents the complete sequence of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multip sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility.
   6976
                                                                                                                                                                                                                                 New nucleic acid sequences from human endogenous retrovirus-W expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnance.
                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis; rheumatoid polyarthritis; insulin-dependent disseminated lupus erythematosus; pregnancy; chromosomal management
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                                                                                                                                                                                                                                                                                                                                                                 98WO-FR01442
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                                           e 511.4; DB 20;
. No. 2.2e-148;
ismatches 42;
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pregnancy; chromosomal marker;
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HERV-W;

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Matches 552; Conserv
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                           Komurian-Pradel, F., Paranhos-Baccala, G., Ounanian-Paraz, A., Sodoyer, M., Ott, C., Re Mallet, F., Mandrand, B. and Perron, H. Molecular cloning and characterization of associated with retrovirus-like particles virology 260 (1), 1-9 (199) 99335590
                                                                                                                                   AF127229 2004 bp mRNA linear VRI Multiple sclerosis associated retrovirus element clone pol-env3'LTR-like mRNA sequence.
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Sequencing vector: Plasmid; n/a; 80% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 176087 bases at least Q40
Consensus quality: 176095 bases at least Q30
Consensus quality: 176095 bases at least Q30
Insert size: 178000; agarose-fp
Insert size: 178000; agarose-fp
Quality coverage: 11.5 in Q20 bases; agarose-fp
Quality coverage: 11.7 in Q20.
* NOTE: This is a 'working draft' sequence. It currently
consists of I contigs: Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zimmer, A. and Zody, M.
                                                                                                                                                                                                 assembly_fragment.
                                                                                                                                                                                                                                              by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 176095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L4296
Center clone name: 497_M_7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; M77815; 32% of reads
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                         /clone="RP11-497M7"
                                                /chromosome="18"
/map="18"
                                                                                                /db_xref="taxon:9606"
                                                                                                                       /organism="Homo sapiens"
/clone_lib="RPCI-11 Human
                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                                     176095:
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Barna,N., Beckerly,R., Beda,F.,
                                                                                                                                                                                                                     be preserved of 176095 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150404 CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAATGACATTGAAGGCACCCCTCCCGAG
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                                                                                                                                                                                                                                                                                                   210336 bp
Homo sapiens chromosome 18 clone
SEQUENCE, 2 unordered pieces.
AC022171
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 210336)
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mararde, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Webb, C., Wilhelmy, J., Yu, S. and Davis, R.W.
Unpublished 2 (bases )
                                                                                                                                                                                                                                                              AC022171.18 GI:13270574
HTG; HTGS_PHASE1; HTGS_D
                                                                                                                                                                                                                   Homo sapiens
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                                                                  CAAATTGTTCTTCAAATGGAGCACCAGATGGAGTCCATGACTAAGATCCACCGTGGACCC 58295
                                                                                                                                                                                     ccctgtatctttaacctccttgttaagtttgtctcttccagaatcaaaactgtaaaacta 60
ctggaccggcctgctagcccatgctccgatgttaatgacattgaaggcacccctcccgag
                                                                                                                                                               CCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATCAAAACCGTAAAACTA 58235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator Big Dye; 88% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 208312 bases at least Q40
Consensus quality: 20817 bases at least Q30
Consensus quality: 209157 bases at least Q30
Consensus quality: 209157 bases at least Q30
Insert size: 199762; agarose-fp
Insert size: 210236; sum-of-contigs
Quality coverage: 8.7x in Q20 bases; sum-of-contigs
Quality coverage: 8.7x in Q20 bases; sum-of-contigs
Quality coverage: 8.7x in Q20 bases; sum-of-contigs
**NOTE: This is a 'working draft' sequence. It currently
**consists of 2 contigs. The true order of the pieces
**is not known and their order in this sequence record is
**arbitrary. Gaps between the contigs are represented as
**runs of N, but the exact sizes of the gaps are unknown.
**This record will be updated with the finished sequence
**as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On I
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Yu, S. and Davis, R
Direct Submission
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Glukhov, S.,
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Sequencing Vector: plasmid; plasmid_accession;
Chemistry: Dye-primer; 10% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: hum-info@sequence.stanford.
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                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig44
clone_end:T7"
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clone_end:SP6"
a 37228 c 37515 g 67816 t
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., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
.,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .66468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
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                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X.,
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Submitted (22-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 30, 2000 this sequence version replaced gi:6087973. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens clone RP11-2N15, WORKING
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Homo sapiens, clone RP11-2N15
                                                                                                                                        Direct Submission
                                                                                                                                                             Wyman,D., Ye,W.J., Zimmer,A. and
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                               Zody, M.
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
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Insert size: 148024; sum-of-contigs
Quality coverage: 3.9 in Q20 bases;
Quality coverage: 4.8 in Q20 bases;
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63442 98587; contig of 35146 bp
98588 98687; gap of 100 bp
98688 148724; contig of 50037 bp
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/note="assembly_fragment"
a 27449 c 27101 g 46463
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2502: gap of 100 bp

7948: contig of 5386 bp in length

8048: gap of 100 bp

15800: contig of 7752 bp in length

15900: gap of 100 bp

25059: contig of 9159 bp in length

25159: gap of 100 bp

41906: config of 16747 bp in length
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                            Submitted (22-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 8339)
                                                                                                                                                                                                                                                                                                       complete sequence. AL162912 AL121824 AL162912.1 GI:740
                                                                                                                                                                                                                                                                                                                                                     Human DNA sequence
                                                                                                                                                                            Direct Submission
                                                                                                                                                                                           Pearce, A.
                                                                                                                                                                                                                                                          Homo sapiens
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following abbreviations are used to associate primary accession bers given in the feature table with their source databases:
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                                                                        AGGACTAGCTGGATTTCCTAGGCCAACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACC 6023
                                                                                             aggactagctggatttcctaggccaacgaagaatccctaagcctagctgggaaggtgact 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sections only once, except for a Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. Rp6-198C4 is from the library Rp01-6 constructed by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPORTANT: This sequence is not the RP6-198C4 It may be shorter because
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http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all
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                                                                                              Direct Submission
Submitted (09-MAY 2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63
On Feb 16, 2001 this sequence version replaced 91:11597125.
                                                                                                                                                                                                                                             Waterston,R.H.
Direct Submission
Submitted (16-FEB-2001) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (27-JUN-2000) Genome
University School of Medicine,
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Sulston, J. E. and Waterston, R.
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Homo sapiens BAC clone RP11-95P9 from 7, complete sequence.
AC073626
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5 (bases
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The sequence of Homo sapiens BAC c
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Center project name: H_NH0095P09
                                    Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                        Center: Washington University Genome Center code: WUGSC
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clone sections once, This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping ections once, or longer because we provide a small overlap neighboring data submissions.

This sequence was all regions were double finished as follows unless double stranded, sequenced v with an alternate

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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome approach Genomics 51-1-8. The clone may be obtained either from libraries. Genomics 51-1-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       base
from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIGHBORING SEQUENCE INFORMATION:
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                      /rpt_family="MaLR" 9047. .9246
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/db_xref="taxon:9606"
/chromosome="7"
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     family="MaLR"
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13026. .13433
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13026. .13357
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13053. .13434
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13035. .13171
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                                                                                                                                                               sequence.
AL583805
AL583805.
Submitted (29 SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 2, 2001 this sequence version replaced gi:14702155.
During sequence assembly data is compared from overlapping clon where differences are found these are annotated as variations
                                                                                  Clark
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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9

RP11-134K1 is from the library RPC1-11.1 constructed by the group of pleter de Jong. For further details see http://www.sanger.ac.uk/HGP/Chme.htm
aggactagctggatttcctaggccaacgaagaatccctaagcctagctgggaaggtgact 360
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This sequence was finished as follows unless otherwise noted: all
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VECTOR: pBACe3.6
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/clone_lib="RPCI-11.1"
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/db_xref="taxon:9606"
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PROGRESS ***, 9 unordered pieces.
AL451130 AC011776
AL451130.7 GI:196477
                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 59% of reads
Sequencing vector: plasmid; LO8752; 40% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Consensus quality: 206696 bases at least Q40
Consensus quality: 208786 bases at least Q30
Consensus quality: 210138 bases at least Q20
Insert size: 211296; sum-of-contigs
Insert size: 183186; 9.1% error; agarose-fp
Ouality coverage: 9.78x in Q20 bases; sum-of-contigs Quality
coverage: 12.66x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 10, 2002 this sequence version replaced gi:18151469. Draft Sequence Produced by Whitehead Institute/MIT Center for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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 2460
2560
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 4743: gap
6823:
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4643:
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               2459: contig of 2459 bp in length
9: gap of 100 bp
4643: contig of 2084 bp in length
3: gap of 100 bp
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Best Local Similarity
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                                                                                                                                                              113538 TGTCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTGAGAGCGGGGACTGAGAGAC 113479
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                                                                                                                                                                                                                                                                                                             CTGGACCGGCCTGCTAGCCCATGCTCCGATGTTAACGACATTGAAGGCACCCCTCCTGAG 113599
                 aggactagctggatttcctaggccaacgaagaatccctaagcctagctgggaaggtgact 360
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/db_xref="taxon:9606"
/chromosome="9"
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94.2%;
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contig of 2229
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9153 9252: gap of 100 bp 10253 198727: contig of 189475 bp in length 198728 198827: gap of 100 bp 198828 202432: contig of 3605 bp in length 202433 202532: gap of 100 bp 202533 206117: contig of 3585 bp in length 206118 206217: gap of 100 bp 206218 209532: contig of 3315 bp in length 209533 209632: gap of 100 bp 209533 209632: gap of 100 bp 209533 209632: gap of 100 bp 209533 209632: gap of 2464 bp in length 209533 209632: contig of 2464 bp in length.
                                                                                                                   /note-"assembly_fragment:03097"
202533: .206117
/note-"assembly_fragment:03385"
206218: .209532
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209633. .212096
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38564 c 41164 g 68462 t
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                                                                                                                                                                                                                                                                                                                                                                                                         Earnhart.C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lux, Lucier,R., Luna,R., Ma,J., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Morgan,M., Morris,S., Muser,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Muserson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Nikerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Noledo,R., Pace,A., Payton,B., Peery,J., Perez,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Syatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agagcacagcgggagggacaaggatcgggatataaacccaggcattcgagccggcaacgg 540
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                                                                                                                                                                                                       Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Walliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Williams, G., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barbaria, J., Benton, J., Éimage, K., Blankenburg, K., Bonnin, D.
Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.,
Buhay, C., Burcel, S., Brieva, M., Burcell, K.L., Byrd, N.C.,
Buhay, C., Burcell, K.L., Burdell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Chen, G., Chen, R., Chen, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Coyle, M.D., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Farnhart F. Edge, C., Carrone, S., Derbin, K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175040)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
                                                                                                                              Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Weinstock,G. and Gibbs,R.
                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 3 clone
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Bryant, N.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113239
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 594;
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TITLE
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                                                                            121 ctggaccggcctgctagcccatgctccgatgttaatgacattgaaggcacccctcccgag 180
                                                                                                                                                                                                                                                             61 caaattgttcttcaaatggagcaccagatggagtccatgactaagatccaccgtggaccc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ccctgtatctttaacctccttgttaagtttgtctcttccagaatcaaaactgtaaaacta 60
                                             CTGGACTGGCCTGCTAGCCCATGATCCGATGTTAATGACATCAAAGGCACCCCTCCCAAG
                                                                                                                                                                                                                    CANATGGGTCTTCAAATGGAGCCCCAGATGCAGTCCATGACTAAGATCCACCACAGACCC 123249
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112178
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140422
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157648
157748
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93.8%;
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0;

Indels

1; Gaps

1;

123189

Length 175040;

Score 560.2; Pred. No. le Mismatches

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Assembly program: Phrap; version 0.990329First findPhrapList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 177002 bases at least Q40 Consensus quality: 181942 bases at least Q20 Consensus quality: 185128 bases at least Q20 Estimated insert size: 180460; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: HBEK Center clone name: RP11-3J2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....- Project Information
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                                                                                                                                                                                                                     /clone="RP11-3J2"
                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                      /chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         47110: contig of 47110 bp in length
47210: gap of unknown length
80061: contig of 32851 bp in length
80161: gap of unknown length
112177: contig of 32016 bp in length
112277: gap of unknown length
140321: contig of 28044 bp in length
140421: gap of unknown length
157647: contig of 17226 bp in length
157747: gap of unknown length
168444: contig of 10697 bp in length
168444: gap of unknown length
175040: contig of 6496 bp in length
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.2; DB 2;
.1e-167;
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                                                                                                                                                                                                                 TITLE
JOURNAL
 Query Match
Best Local
                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aggactagctggatttcctaggccaacgaagaatccctaagcctagctgggaaggtgact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | gaaltotcaactgcacaacccctactatgccccaattcagcgggaagcagttagagcggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGACTAGCTGGATTTCCTAGGCCAACTAAGAATCCCTAAGCCTAGCTGGGAAGGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAATCTCAACTGCCCAACCCCTACTATGCCCCAATTCAGCAGGAAGCAGTTAGAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens geno
LL56-APP region,
AP001538
AP001538.1 GI:73
                                                                                                                                                  Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamhhara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                   l (bases 1 to 174019)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 174,019 genomic DNA of 21q21.1-q21.2
Published Only in DataBase (2000) In press
2 (bases 1 to 174019)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                             Direct Submission
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens genomic DNA, chromosome -APP region, complete sequence.
                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                      sapiens DNA,
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/chromosome="21"
/clone="8853K11"
/map="21q21.1-q21.2"
a 31416 c 32248 g 57052
                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                 Metazoa;
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87.7%;
93.7%;
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                                                                                                                                                                                                                                                                                                                                   Primates; Catarrhini;
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Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                            174019 bp
556.6; DB 9;
No. 1.5e-166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633
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Homo sapiens genomic DNA, chromo
AP001674 AL163219 BA000005
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2 (bases 1 to 340000)
Hattori,M., Fujiyama,A., Taylor,T.D., Watanabe,H., Yada,T.,Hattori,M., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K., Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
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_"ILMA4A" family="LINE/L1" type=DISPERSED	A4A" -"LINE/L1" DISPERSED	.l" 3X11, 5' partial" *"RPCI-11 BAC library"	/note="Accession No. AP001538" /organism="Homo sapiens" /db_xref="taxon 9606" /chromosome="21"	9918, 5' partial" "RPCI-11 BAC library"	/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="21"	= 0	URL: http://chr21.rz-berlin.mpg.de/ .163219: Submitted (10-Apr-2000). Location/Qualifiers 1340000	tute for Molecular Genetics, D-14195 Berlin, Germany, 21@molgen.mpg.de	* GBF, Dept. of Genome Analysis, * Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail: info.genome@gbf.de * URL: http://genome.gbf.de/	University School of Medicine, Molecular Biology, * Tokyo 12, Japan, 11: nshimizu@dmb-med.keio.ac.jp http://www.dmb.med.keio.ac.jp/	* Institute of Molecular Biotechnology, Genome Analysis, * Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de * URL: http://genome.imb-jena.de/ and	On May 30, 2000 this sequence version replaced gi:7717271. The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan, * e.mail: hattori@gsc.riken.go.jp * URL: http://ngp.gsc.riken.go.jp/	Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below)	<pre>Zimmermann, W., Rosenthal, A., Kudoh, J., Shibuya, K., Kawasaki, K., Asakawa, S., Shintani, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Bloecker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmaeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and Yaspo, M.L.</pre>	vald, K., Rump, A., Schillhabel, M., Schudy, A.,
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Pred. No. 1.7e-166;
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27321 ACTAAATCTTGCAACTGCA 27303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel:81-42-778-9923, Fax:81-42-778-9924)
On Jul 14, 2000 this sequence version replaced gi:8117383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp, UKL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
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DRAFT SEQUENCE, 13 unordered
APO01545
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and
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1 (bases 1 to 149755)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 149,755 genomic DNA of 18921

Published Only in DataBase (2000) In press

2 (bases 1 to 149755)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 145596 bases at least Q40
Consensus quality: 147102 bases at least Q30
Consensus quality: 147910 bases at least Q30
Consensus quality: 147911 bases at least Q30
Insert size: 148555; sum-of-contigs
Quality coverage: 10.98x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                  Center project name: HumDraft18 Center clone name: RP11-762G24
                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://hgp.gsc.riken.go.jp/
Contact: hattor1@gsc.riken.go.jp
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: RIKEN
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sapiens DNA, clone:RP11-762G24.
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NOTE: This is a 'working draft' sequence. It currently consider in this sequence record is arbitrary. Gaps between the control are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence are unknown. preserved NOTE: 44929 82703 101445 116306 123885 130456 133720 137517 144452 146768 148320 141641 44828 contig of 82602 contig of 101344 contig of 116205 contig of 123784 contig of 133619 contig of 137416 contig of 137416 contig of 141540 contig of 144551 contig of 146667 contig of 148219 contig of St b draft' 44828 37674 18642 14761 7479 6471 3164 3697 4024 2711 2216 'n 'n length length length length length
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133720. .137416
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130456. .133619
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149755: cont
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141540: cc
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91.8%;
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contig of 1452 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccetgtatctttaacctccttgttaagtttgtctcttccagaatcaaaactgtaaaacta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcatccacctctaaacatggggcttgcaacttagctcacacccgaccaatcagagagctc 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aggactagctggatttcctaggccaacgaagaatccctaagcctagctgggaaggtgact 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTCAGAGGGGGGTACTGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catcagccaacctccccaacagcacttgggttttcctgttgagagggggggactgagagac 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caaccccctttgggtccccttccctttgtatgggcgctctgttttcactctatttcactct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaaatctcaactgcacaacccctactatgccccaattcagcgggaagcagttagagcggt 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAACCCCCTTTGGGTCCCCTCCCTTTGTATGGGAGCTCTGTTTTCACTCTATTAAATCTT 6766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agagcacagcgggagggacaaggatcggggatataaacccaggcattcgagccggcaacgg
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boyuslavki, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Johnson, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacCean, C., MacGonald, P., McCarthy, M., McEwan, P., McKernan, K., McChan, S., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McCPan, M., McCevan, P., McKernan, K., McCPan, C., MacGen, C., Marden, C., MacGen, C., McCerthy, M., McEwan, P., McKernan, K., McCPan, C., MacGen, MacGen, C., MacGen, MacGen, MacGen, C., MacGen, MacGen, MacGen, MacGen, MacGen, MacGen, MacGen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 18 clone SEQUENCE, 3 unordered pieces. AC090313
                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Pr
1 (bases 1 to 152775)
Birren,B., Linton,L.,
                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                          Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 18, clone RP11-762G24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC090313.2 GI:14971265
HTG; HTGS_PHASE1; HTGS_
                                                                                                                                                                                                                                                                                                        (bases 1 to 152775)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA linear
RP11-762G24 map 18,
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WORKING DRAFT
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O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,
Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Travers, M., Travis, N., Trigilio, J., Vassilev, H., Viel, R., Vo, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 20, 2001 this sequence version replaced gi:12957949. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson, B., Wu, X., Wyman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 15,319 bases at least Q40
Consensus quality: 15,2154 bases at least Q30
Consensus quality: 15,2385 bases at least Q20
Insert size: 146000; agarose-fp
Insert size: 152575; sum-of-contigs
Quality coverage: 8.0 in Q20 bases; sum-of-contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L12582
Center clone name: 762_G_24
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149190 152775: contig of 3586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:
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7712 7811: gap of 100 bp
7812 149089: contig of 141278 bp in length
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                                                                                                                                       /note="assembly_fragment" 149190. .152775
                                                                                                                                                                                               vector_side:left"
7812. .149089
                                                                            clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-762G24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                       note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                          clone_lib="RPCI-11 Human Male"
                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome="18"
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Query Match

98

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Score

551.8;

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Length 152775;

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JOURNAL
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                                                                   REFERENCE
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                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108801 GCATTCACCTTTAAACACGAGGCTTGCAACTTAGCTCACACCTGACCAATCAGAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108681 CATCAGCCAACCTCCCCAACAGCACTTGGGTTTTCCTGTTCAGAGGGGGGTACTGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108621 GAAATCTCAACTGCACAACCCCTACTATGCCCCAGTTCAGCAGGAAGCAGTTAGGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108561 CTGGACCAGCCTAGCCCATGCTCCGATGTTAATGACATCGAAGGCAACCCTCCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     541 caaccccctttgggtccccttccctttgtatgggcgctctgttttcactctatttcactct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 agagcacagcgggagggacaaggatcgggattataaacccaggcattcgagccggcaacgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 catcagccaacctccccaacagcacttgggttttcctgttgagagggggggactgagagac
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Homo sapiens chromosome 5 clone
AC093531
AC093531.2 GI:16945981
Submitted (16-NOY-2001) DOE Joint Genome Institute, Drive, Walnut Creek, CA 94598, USA
                                                                 Submitted (31-AUG-2001) Production Sequencing Genome Institute, 2800 Mitchell Drive, Walnut 3 (bases 1 to 163803)
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DOE Joint Genome Insti
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                                 Direct Submission
                                                 DOE Joint Genome Institute and Stanford Human Genome Center.
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                                           116808 CAACCCCCTTTGGGTCCCCTCCCATTGTATGGGAGCTCTGTTTTCACTCTATTTCACTCT 116749
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          attaaatcttgcaactgaa 619
ATTAAATCTTGCAACTGCA 116730
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Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.3.
Location/Qualifiers
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Sequence Produced by DOE Joint Genome Institute
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/db_xref="taxon:9606"
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Pred. No. 5e-165;
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BE019603 ba84 f03.9
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BE677445 6025944 9
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B1052559 RC5-GN028
B1052559 RC5-GN028
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VERSION
KEYWORDS
SOURCE
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1 (bases 1 to 723)

Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AU138405
AU138405.1
                                                                                                                                                        Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                            HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
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/clone_lib="pLACE1"
/tissue_type="placenta"
/note="vector: pME18SFL3"
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PLACE1 Homo sapiens
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DNA sequence.
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679; Conserv
                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 631)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, I
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., (Yenter, J.C.)
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        Use of a random human
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Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Ge
                                                                                                                                                                                                                                                                                                                                  TCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTTAGCAATACTATAGACAC
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/note="Vector: pBeloBAC11;
/note="Vector: pBeloBAC11;
CalTech Human BAC Library |
a 189 c 99 g 161 |
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/db_xref="taxon:9606"
/clone="2506C15"
/clone_lib="CITBI-E1"
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                          CTGTGGTACCTCAGCCTATCGTTGTTTGAATGGCTCTTCAGAATCTATGTGCTTCCTCTC
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AU138097 PLACE1
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,)
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Takao Isogai
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Mammalia; Eutheria; Primates;
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173 c 131 g 189
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Pred. No. 1.5e-156;
0; Mismatches 37;
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National Institutes of Health, Mammalian
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Tissue Procurement: ATCC
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                                     194
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/lab_host="pHIOB (phage-resitant)"
/lab_host="pHIOB (phage-resitant)"
/note="organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the place to th
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                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 586)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                 Homo sapiens
cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing
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/clone_1ib="NIH_MGC_21"
/clone_1ib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
/note="Organ: placenta; Vector: pOTB7; Site_susing the pirectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 427)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Marti,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson,RK.
                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 410.
Location/Qualifiers
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4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
/with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. 1st strand cDNA was primed
                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:1390111"
/db_xref="taxon:9606"
/clone="IMAGE:453755"
                                                                                                                                                         /dev_stage="20 week-post conception fetus"
                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                 /clone_lib="Soares_fetal_liver_spleen_lNFLS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone from S. Wiemann, Molecular Genome Analysis, German Can
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cD
sequencing consortium of the German Genome Project. No sl se
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DKFZp313K157_r1 313 (synonym: h
DKFZp313K157 5', mRNA sequence.
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                                                                                                                                       Contact: Ottenwaelder B
                                                                                                                                                       Unpublished (2001)
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hes 23;
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Proc. Nat
99380589
                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 586)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a
                                                                                                                                                                                     AQ776289

AQ776289

HS_5528_A2_B10_T7A RPCI-11 Human Male BAC Library Homo genomic clone Plate=1104 Col=20 Row=C, DNA sequence.

AQ776289

AQ776289.1 GI:5656017

GSS.
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           Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                        Homo sapiens
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/db_xref="taxon.9606"
/clone="DKFZp313K157"
/clone="lbF"313 (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="PH10B"
/note="Vector: pTriplEx2; Site_1: SfcDNA-collection"
1 a 132 c 156 g 209 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contact the RZPD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charlottenburg, GERM Location/Qualifiers
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94.8%;
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GERMANY; Email: clone@rzpd.de.
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                                                                       cctctcattcttagtgccccctatgaccatctacactgaaccaagatttatacaatcatgt 926
                                                                                                                                                                                                                                                                                                                                                                                                                  tttgtctgtggtacctcagcctatcattgtttgaatggctcttcagaatctatgtgctt 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccaatgcatcaggtgggtaacacctcccacacgaatagtctgcctaccctcaggaatatt 806
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                    agatcaacttaactccctagcagcagtagtccttcaaaatcgaagagctttagacttgct
                                                                                                                                                                            gctaggcagactaggtactggcattggcagtatcacaacctctactcagttctactacaa 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAATGCATCAGGTGGGTAACTCCTCCCACACGCATAGTCTGAGT - CCNTCAGGAATATT
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                                                                                                                                                        GCTAGGCAGACTAGGTACTGGCATTGGCAGTATCACAACCTCTACTCAGTTCTACTACAA 182
                                                                                                                                                                                                                                                                         cgtacctaagccccacaacaaaagagtacccattcttccttttgttatcagagcaggagt 986
                                                                                                                                                                                                                                                                                                                CCTCTCATTCTTAGTGCGCCCTATGATCATCTACTCTGAACAAGATTTATACAATTATGT
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  AGATCAACTTAACTCCCTAGCAACAGTAGTCAATCACNATCGAAGAGCTTTAGACTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Washington
401 Queen Anne Avenue North, Sea
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 586.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.htsc.washington.edu
Plate: 1104 row: C column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones are derived from the human BAC library RPCI-11. For BAC
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High Throughput Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="Plate=1104 Col=20 Row=C"
/clone_lib="RPCI-11 Human Male BAC Library"
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/db_xref="taxon:9606"
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87.2%;
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Pred. No. 4.8e-88;
Pred. No. 4.8e-85;
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                673 tccaatctggaaataacccatacctcaaacctcacctgtgtaaaatttagcaatactata 732
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61
                                                                     1 CAATGGAACAACTTCAGCACAGAAATAAACACCACTTCCGTTTTAGTAGGACCTCTTGTT 60
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TCCAATCTGGAAATAACCCATACCTCAAACCTCACCTGTGTAAAATTTAGCAATACTACA
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Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holma, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterst, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R68740 459 bp mRNA linear EST 26-JUN-179: yi14g06.rl Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139258 5' similar to SP:B44282 B44282 RETROVIRUS-RELATED ENV POLYPROTEIN - ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stops: 316
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1644 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 316.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
Insert Size: 1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="GDB:545824"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares placenta Nb2HP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:139258"
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                                                                                                                                                           24.1%;
91.3%;
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                                                                                                                                        Score 356.4; DB 1
Pred. No. 4.5e-84;
0; Mismatches 36
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                                                                                                                                                                    Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 979 row: I column: 3
Seq_primer: T7
                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 608) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.
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                                                                                                                            quality sequence stop:
Location/Qualifiers
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen d
and partially digested with a combination of EcoRI and
                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=979 Col=3 Row=I"
/clone_lib="RPCI-11 Human Male
/sex="male"
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Adams,M.D.
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AAGCTGTAAAGCTACAAATGGCTCTTCAAATGGAGCCCCA 151
                                                         TACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTTTTAAGTTTGTCTCTTCCAGAATTG
                                                                          tactcctctttggaccctgtatctttaacctccttgttaagtttgtctcttccagaattg
                                                                                                                      TCAGCCAATGGATGCCCTGGATTCTCCCCTTCTTAGGACCTCTAGCGACTATAATACTGT
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BG004254 41 RC6-GN0070-301100-014-C06 G BG004254 BG004254 GI:12445242 EST. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 411)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jonganeel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and Tel: +55-11-2704922 Fax: +55-11-2707001 Shotgun sequencing 20202663 sequence tags Simpson, A.J. Homo sapiens Natl. Acad. asimpson@ludwig Sci. of the human transcriptome with ORF .org U.S.A. 411 bp GN0070 br. 97 (7), Homo andar, mRNA sapiens cDNA, 01509-010, linear (2000) Sao Paulo-SP, mRNA sequence. EST 24-JAN-2001 expressed

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l (bases 1 to 382)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                      BI052569 382 bp mRI
RC5-GN0282-220101-011-G04 GN0282 Homo
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                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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96 g 118 t
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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Pred. No. 9.3e-84;
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Local Similarity
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                    tcccacacgaatagtctgcc 790
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC5&t2=RC5-GN0282-
220101-011-G04&t3=2001-01-22&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 381.
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Laboratory of Cancer Genetic
Ludwig Institute for Cancer
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Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xref="taxon:9606"
/clone_lib="GN0282"
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Pred. No. 2.8e-82;
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gtaggacctcttgtttccaatctggaaataacccatacctcaaacctcacctgtgtaaaa
                                                                                                                      acccatactcgcctggtgagcctatttaataccaccctcactcggctccatgaggtctca 537
                                                                                                                                                                                                                                                                                 gcccaaaaccctactaactgttggatgtgcctccccctgcacttcaggccatacatttca
                                                                                                                                                                                                                                                       GCCCAAAACCCTACTAACTGTTGGATATGCCTCCCCCTGAACTTCAGGCCATATGTTTCA
                                                                                                                                                                                                                                                                                                                                                                                    ACCCATACTCGCCTGGTAAGCCTATTTAATACCACCCTCACTGGGCTCCATGAGGTCTCG
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-GN0282-210201-013-G04&t3=2001-02-21&t4=1)
Seq primer: puc 18 forward
Seq primer: puc 18 forward
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
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Location/Qualifiers
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/note="Organ: placenta_normal; Vector: Pucl9: Site_2: SmaI
/note="Organ: placenta_normal; Vector: Pucl9: SmaI
/note="Organ: placenta_normal; Vector: pucl8; Site_1: SmaI
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                                                                           357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2-RC5-GN0282-
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1 (bases 1 to 373)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Coldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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                                                                                          Similarity
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                                                                                                                                                                              /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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US-09-011-745-8
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NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-9224
TELEPAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
IFNORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
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Patent No. 5
                                                                                                                                                      Query Match
Best Local Similarity
Matches 184; Conserv
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APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED P
TITLE OF INVENTION: ENCODING TUNDMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       MOLECULE TYPE:
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STREET: 87 Cambr.
CITY: Cambridge
STATE: Massachus
COUNTRY: U.S.A.
ZIP: 02140
462
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STRANDEDNESS:
TOPOLOGY: lin
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Lavallie, Edward
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CambridgePark Drive
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                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
S-08-721-489-2
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 876-58: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION UMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 542 base pairs
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ADDRESSEE: Genetics Institute,
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TYPE: nucleic acid
STRANDEDNESS: doubl
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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ACCTTCACTGCCCACACCCAT 542
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Treacy, Maurice
Spaulding, Vikki
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- NO: 2:
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ENCODING
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91.5%;
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Pred. No. 1.4e-46;
0; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 302
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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                                                                                                                                      1120
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NAME: Berridge, William P.
REGISTRATION NUMBER: 30,03
REFERENCE/DOCKET NUMBER: V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
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CORRESPONDENCE ADDRESS:
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1240 gtcactgagaaagttaaagaaattcgagatcgaatacaatgtagagcagaggagcttcaa 1299
                                                                     1180
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                                                                                                                                                                                                                                          406
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700 South Washington Street,
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Frederic BEDIN
Glaucia PARANHOS-BACCALA
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55.7%;
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
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Pred. No. 4.1e-37;
0; Mismatches 234;
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US-08-691-563C-46
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INFORMATION FOR SEQ ID NO: 46:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
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1036 ttctactacaaactatctcaagaaataaatggtgacatggaacaggtcactgactccctg 1095
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1859 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 38588
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/691,563C
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: BETTINGER, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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APPLICANT: Florence KOMURLAN-PRADEL
APPLICANT: COLette JOLIVET
APPLICANT: Bernard MANDRAND
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APPLICANT: Frederic BESI
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22314
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                                                      Local Similarity
mes 257; Conserv
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                                                         Conservative
                                                                                                                                                                                                                                                         single
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                                                                        8.98;
                                                   Score 131.2; 1
Pred. No. 2e-3;
0; Mismatches
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                                                                        TELEX: 248345
INFORMATION FOR SEQ ID NO:
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                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                       TELEPHONE: /U5 1.05050
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                    1704 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPATIBLE PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: YANAGIDA, NOBORU
TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: RECOMBINANTS EXPRESSING THE ENVEI
TITLE OF INVENTION: AVIAN RETICULOENDOTHELIOSIS RETR
NUMBER OF SEQUENCES: 2
                                                                              CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERALD M.
REGISTRATION NUMBER: 28,977
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WITTER, RICHARD L.
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                                                                                ; ORGANISM: Nucleotide US-09-078-294-4
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 Query Match
Best Local S
Matches 263
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 4
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Best Local Similarity
Matches 268; Conserv
                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09078294 Patent No. 6265211
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
                                                                                                                                                                                            CURRENT FILING DATE: 1998-05-13
                                                                                                                                                                                                                                                                                          APPLICANT: Choo,
                                                                                                              LENGTH: 80246
TYPE: DNA
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HYPOTHETICAL: NO
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                    Similarity
   Conservative
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Pred. No. 9.2e-28;
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Score 114.8; D
Pred. No. 3.8e-
0; Mismatches
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                                                                                                                                                                    ; LOCATION: (1); OTHER INFORMATION: n is US-09-011-745-1
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SEQ ID NO 1
LENGTH: 2518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09011745 Patent No. 6165715
                                                                         Best Local Similarity 55.(
Matches 224; Conservative
                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: PCT/GB96/02061 EARLIER FILING DATE: 1996-08-23
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                                                                                                                                                                                                                                                                                  TYPE: DNA
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aaattatcccatcagttaatatctgatgtccaagtcttatccggtaccatacaagattta 1893
                         aaactatctcaagaaataaatggtgacatggaacaggtcactgactccctggtcaccttg 1104
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                                                                       7.7%; Score 114.2; DB 4; 55.0%; Pred. No. 8e-27; ative 0; Mismatches 183;
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                                                                                                            Length
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APPLICANT: Collins, Mary KL
APPLICANT: Wedss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER APPLICATION NUMBER: DET/GB96/02061
EARLIER APPLICATION NUMBER: B9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
ROPETMINE, DETAILS VILLE
FOR THE PORT OF 
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US-09-011-745-8
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Patent No. 6165715
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LENGTH: 5865
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OTHER INFORMATION:
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OTHER INFORMATION: n is
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LOCATION: (3612)
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; SEQ ID NO 3
; LENGTH: 80595
; TYPE: DNA
; ORGANISM: Nucleotide s
US-09-078-294-3
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; OTHER INFORMATION: n is
US-09-011-745-8
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Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
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                                                                y Match 6.1%;
Local Similarity 57.5%;
hes 206; Conservative
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tggcagcagtgactctccaaaaccgctgaggcctagactctcatgttgagaaaggaag--
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Pred. No. 1.3e-26;
0; Mismatches 183
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                                                                              DB 4;
.4e-18;
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US-09-011-745-9
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APPLICANT: COllins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09011745 Patent No. 6165715
                                                                                                                         NAME/KEY: misc_feature
LOCATION: (3913)
OTHER INFORMATION: n is any
-09-011-745-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                   LOCATION: (3912)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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LOCATION: (3911)
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                                              Local Similarity 49.3
mes 224; Conservative
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                                            Score 70; DB 4; Length 3925;
Pred. No. 2.4e-12;
0; Mismatches 215; Indels
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                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 5
                                                                                                                                                                                                                                             OTHER INFORMATION:
OTHER INFORMATION:
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GENERAL INFORMATION:
APPLICANT: COLLINS, MARY KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER APPLICATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
         PEATURE: misc_feature LOCATION: (3777)
                                                                                NAME/KEY: misc_feature
LOCATION: (3776)
OTHER_INFORMATION: n is
                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (3775)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
LOCATION: (3774)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
OTHER INFORMATION: n is
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; LOCATION: (3965)
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US-09-011-745-5
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                                                                                                                                                                                   Sequence 1, Application US/08766528 Patent No. 6190861
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                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Jay A.
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NAME/KEY: misc_feature
'CCATION: (3962)
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                                                                                 APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
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 STALL: USA COUNTRY: USA 02109-1875
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                                                         Boston
  READABLE FORM
                                         Massachusetts
                                                                     60 State Street
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Pred. No. le-11;
0; Mismatches 2
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                                                                                                                                           SWINE
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                                                                                                                                           RETROVIRUS
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; Sequence 5, Application
; Patent No. 6033905
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MOLECULE TYPE:
US-08-766-528-1
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Best Local Similarity
                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                         PRIOR APPLICATION DATA:
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                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 8060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER: PCT, FILING DATE: 06-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                     SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/716,351A
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1703 GATCATTCAGGGGCCATCAGAGACTCCATGAACAAACTTAGAGAAAGGTTGGAGAAGCGT 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1583 GAGGAATCCCTAACCTCCTTATCTGAAGTAGTCCTACAGAATAGAAGAGGGGTTAGATTTA 1642
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ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caagatcaacttaactccctagcagcagtagtccttcaaaatcgaagagctttagacttg 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcagaggagcttcaaaacaccgaacgctgg 1314
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14-DEC-1995
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53.3%;
                                                                                                                                                                                                                                                                                 Retroviral Vectors
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PCT/US94/03784
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ATTORNEY/AGENT INFORMATION:

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US-08-258-420-8
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Best Local Similarity
Matches 128; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nienhuis, Arthur W. APPLICANT: Vanin, Elio F. TITLE OF INVENTION: No. 5710037el NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6919
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TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-9643
FORMATION FOR SEQ ID NO: 5:
                                                  APPLICATION NUMBER: US/0
FILING DATE: 10-UUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                        OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1087 gactccctggtcaccttgcaagatcaacttaactccctagcagcagtagtccttcaaaat 1146
ATTORNEY/AGENT INFORMATION:
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CITY: F
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LOCATION: 1..10970
OTHER INFORMATION: /standard_name=
OTHER INFORMATION: vector"
                                                                                                                                                                                             COMPUTER:
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                                       FILING DATE
                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                  Roseland
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Bastian, Kevin L.
Bastian, 34,774
                                                                                                                                                                                                                                                                                New Jersey
                                                                                                                                                                                                                                                                                                                 6 Becker Farm
                                                                                                                                                                                                                                                                  USA
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∑: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                     Carella, Byrne,
                                                                                                                                                                                                               inch diskette
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                                                                                                                       US/08/258,420
                                                                                                                                                                                                                                                                                                                   Road
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Pred. No. 1.9e-11;
0; Mismatches 100
                                                                                                                                                                                                                                                                                                                                   Bain,
                                                                                                                                                                                                                                                                                                                                                                                    Retroviral Envelope
                                                                                                                                                                                                                                                                                                                                   Gilfillan, Cecchi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "p537 retroviral
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                                                                                                                                                                                                                                                                                                                                                                                      and LTR and Retroviral Vecto
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Best Local Similarity
Matches 227; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                     1537
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REFERENCE/DOCKET NUMBER: 27
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                               1435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
FEATURE:
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                                                                                                                                                                                                                                                                                         agaattgaagctgtaaagctacagatggtcttacaaatggaacccca 1481
                                                             TTACTGATCTTACTCTTTGGACCTTGCATTCTCAATCGATTAGTCCAATTTGTTAAAGAC 1836
                                                                                                                                 AATAGATCCCCCTGGTTTACCACCTTAATCTCCACCATCATGGGACCTCTAATAGTACTC 1776
                                                                                                                                                                                                                                                                                                                                                        AGGCTTAATCAGAGACAAAAACTATTTGAGACAGGCCAAGGATGGTTCGAAGGGCTGTTT
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                                                                                 atattgttactcctctttggaccctgtatctttaacctccttgttaagtttgtctcttcc 1434
                                                                                                                                                                                                                                                                  TGTTGTTTTTATGCAGACCACACGGGGCTAGTGAGAGACAGCATGGCCAAATTAAGAGAA 1656
AGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCAACAATATCACCA 188:
                                                                                                                                                                                                                                                                                                                                     AGAGGCCTAGATTTGCTATTCCTAAAGGAGGGAGGTCTCTGCGCAGCCCTAAAAGAAGAA
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linear
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Search completed: June Job time: 8391 sec 20, 2002, 09:38:01

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DNA encoding an en
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encoding nove	AAS92666		1929	38.1	6 <u>4</u>	4
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bone m	AAK43040		792	48.4	16.	9
brain e	AAK17251		792	œ	16.	8
Probe #14338 for g	ABA35872		792	œ	716.6	27
1	ABA68919	22	792	8	16.	
n breast cell	ABA50940	22	792	48.4		
oding no	AAS84210	23	(4)	0	4	4
5' non coding, 3'	AAA59209	21	1948	75.4	1116.4	3
endogenous	AAX25659	20	4	75.4	16.	ະ
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Complete human end	AAX25665	20	58	9	1322.6	0

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ALIGNMENTS

RESULT AAV43217 Multiple sclerosis associated retrovirus; MSRV; MS; gag gene; env gene; rheumatoid arthritis-associated AAV43217; (INMR) BIO MERIEUX. 04-JUN-1998. W09823755-A1 Multiple sclerosis associated retrovirus Multiple sclerosis associated retrovirus fragment 5 29-DEC-1998 (first entry) AAV43217 standard; cDNA; 1481 BP 26-NOV-1996; 26-NOV-1997; 96US-0756429 97WO-IB01482 Location/Qualifiers arthritis-associated virus; ss

Human endogenous

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Matches
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       cctgttcctgaacaatggaacaacttcagcacagaaataaacaccacttccgttttagta
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                                                                                              The present sequence encodes an envelope protein of MSRV-1. The envelope protein expressed by the endogenous human retrovirus MRSV-1 has superantigen activity associated with autoimmune disease. The protien can be detected using the method of the invention. The specification describes a process for detecting activity of a superantigen in a biological sample. The process comprises identifying large scale expansion or loss of lymphocytes that carry at least one of the Vbetal6 and/or Vbetal7 determinants. The method is used to screen for agents that inhibit the superantigen, especially those associated with MRSV-1 which is implicated in autoimmune disease, particularly multiple sclerosis. These agents are potentially useful for treatment or prevention (e.g. as vaccines) of autoimmune diseases.
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98US-0175928
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Query Match
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                                                                                                     treating, preventing or ameliorating medical conditions in humans and animals. Detection of the levels of the proteins can be used for the diagnosis of e.g. pre-eclampsia, placental pathology or cancer. Agents which modulate the expression or function of the proteins may be used for treating a neoplastic disease and inhibiting metastasis. Other suggested activities include nutritional activity (e.g. in feeds), cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopolesis regulating activity, tissue growth activity, activin/habibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotide sequences are also stated to be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                      This is the human secreted protein AJ172_2 nucleotide sequence, obtained from a human adult testes cDNA library. The invention relates to secreted human and murine proteins. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for
                                                                              Sequence
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envelope protein; multiple sclerosis-related superantigen; vaccine; surface antigen; transmembrane; multiple sclerosis; neuroprotective; antisense-therapy; autoimmune disorder; ds.
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New human retrovirus HERV-W ENV proteins/peptides having superantigen activity useful for diagnosing and treating multiple sclerosis -

Claim 13; Fig 10; 94pp; English.

On the basis of the PBS t-RNA motif used for the classification of human CC endogenous retrovirus (HERV9) the full length endogenous provirus which CC was been located on the long arm of human chromosome 7 (7921-22) has been CC designated HERV-W. The present invention describes proteins or peptides (I) having superantigen (SAq) activity comprising the ENV protein (ENV) CC of HERV-W, the surface protein (SU) and transmembrane (TM) sub-units. (I) CC have neuroprotective activity, and can be used in: vaccines; antisense-cc useful for diagnosing multiple Sclerosis (MS) or HERV-W-associated CC with MS, substances capable of binding to a retroviral superantigen associated cc with MS, substances capable of blocking transcription or translation of HERV-W retroviral SQG against HERV-W retroviral SQG is useful in therapy. Mucleic acid copable of blocking transcription or translation of HERV-W retroviral SQG is useful in therapy. Nucleic acid copable of blocking SAg activity, capable of binding to a retroviral SQG capable of blocking SAg activity, capable of binding to retroviral SQG is useful in therapy. Nucleic acid copable of blocking SAg activity, capable of binding to a retroviral CC capable of blocking SAg activity, capable of binding to a retroviral CC capable of blocking SAg activity, capable of binding to a retroviral CC capable of blocking SAg activity, capable of binding to a retroviral CC capable of blocking SAg activity, capable of binding to a retroviral CC capable of blocking SAg activity, capable of binding to a retroviral cord copactivity, capable of binding to a retroviral cord capable of blocking transcription or capable of binding to a retroviral cord capable of binding to a retroviral capable of binding to a retroviral capable of binding to a retroviral capable of b

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The present sequence encodes a human endogenous retrovirus envelope protein. The specification describes a method for detecting expression of an envelope protein from a human endogenous retrovirus (HERV), in cells, of a tissue or culture. The method comprises detecting syncytia formation due to the fusogenic properties of the envelope protein. Envelope polypeptides and polynucleotides are used to produce therapeutic or prophylactic compositions, particularly for treatment of cancer, to correct defects in placental development (or other natural formation of other types of syncytia), and to promote adhesion of cells

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Disclosure;

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                                             accttcactgcccacacacacacgccaactgctatcactctgccactctttgcatg
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under pasts of the PBS t-RNA motif used for the classification of human endogenous retrovirus (HERVs) the full length endogenous provirus which was been located on the long arm of human chromosome 7 (7921-22) has been designated HERV-W. The present invention describes proteins or positive (I) having superantique (SAC) positions or positions.
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                                                                                                                                                    Claim
                                                                                                                                                                                            New human retrovirus HERV-W ENV proteins/peptides having superantigen activity useful for diagnosing and treating multiple sclerosis -
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ope protein; multiple sclerosis-related superantigen; vaccine;
ce antigen; transmembrane; multiple sclerosis; neuroprotective;
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t+ (pos:790.792,aa:Phe)
t+ (pos:793..795,aa:Thr)
t+ (pos:812..814,aa:Leu)
t+ (pos:818..820,aa:Ser)
t+ (pos:862..864,aa:Tyr)
t+ (pos:865..867,aa:Gln)
t+ (pos:1174..1176,aa:Arg)
t+ (pos:1174..1176,aa:Leu)
t+ (pos:1174..1176,aa:Leu)
t+ (pos:1174..1176,aa:Leu)
t+ (pos:1174..1176,aa:Leu)
t+ (pos:1174..1176,aa:Leu)
t+ (pos:2017..2019,aa:Lys)
t+ (pos:2017..2019,aa:Arg)
t+ (pos:2028..2028..aa:Arg)
t+ (pos:2028..2021.aa:Arg)
t+ (pos:2039..2021.aa:Gln)
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of HERV-W, the surface protein (SU) and transmembrane (TM) sub-units. (I) have neuroprotective activity, and can be used in: vaccines; antisense-ct therapy; and HERV-W SAg activity-inhibitors. (I) and encoding DNA/RNA are useful for diagnosing multiple scherosis (MS) or HERV-W-associated CC disorders. (I) are also useful for identifying substances (and optionally recovering) capable of binding to a retroviral superantigen associated CC with MS, substances capable of blocking SAg activity and substances capable of blocking SAg activity and substances compable of blocking SAg activity and substances codevoid of SAg activity and substances codevoid of SAg activity and substances codevoid of SAg activity and specific derived from (I), modified to be consist HERV-W retroviral SAg is useful in therapy. Nucleic acid completes encoding (I) are useful as vaccines against MS. Substances capable of blocking SAg activity, capable of binding to a retroviral superantigen associated with MS, or capable of blocking transcription or translation of MS. (I) and nucleic acids encoding them are useful for the treatment and companies of MS. (I) and nucleic acids encoding them are useful for constances codes of specifically claimed envelope protein of HERV-W designated G.
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Sequence 2782 BP; 741 A; 768 Ç 564 G; 709 Ή. 0 other;

Best Local Similarity 92.7 Matches 1373; Conservative

88.3%; 92.7%;

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Query Match
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                                                                                                                         This sequence represents clone cl.PH74 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes
                                                                                                                                                                                                                                                            Claim
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Best Local Similarity
Matches 1372; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an endogenetic retroviral nucleic acid fragment, which is associated with an autolimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autolimnune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosts of autolimnune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro.
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Query Match Best Local S Matches 1218

Local Similarity nes 1218; Conser

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The invention relates to a spatially-addressable set of single exon cc nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting ct the probes with a collection of detectably labelled nucleic acids cound to each probe of the microarray. The probes are useful for cc verifying the expression of regions of genomic DNA predicted to cc encode proteins. They are useful for gene discovery, and for cc determining predisposition and/or prognosing breast disease. Gene cc expression analysis is useful for assessing the toxicity of chemical cc diversity of probes for measuring gene expression, with far less bias ct than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The C contest sequence is a single exon nucleic acid probe of the invention. Cc present sequence is a single exon nucleic acid probe of the invention. Cc printed specification, but was obtained in electronic format directly crown with part of the contest of the microarray contest of the invention.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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2000US-0207456.
2000US-0608408.
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2000US-0234687.
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Matches 1218; Conserv
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                             measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1245
                                                                                                                                                                                                                                                  Claim
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                    224
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1 (bases 1 to 1481)

Ott.C. and Bedin,F.

Ott.C. and Bedin,F.

RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES PATENT: WO 9902666-A 9 21-JAN-1999;

BIO MERIEUX (FR); OTT CATHERINE (FR)

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ORGANISM	VERSION KEYWORDS SOURCE	DEFENET ION	LOCUS	RESULT AL390039	Db 189	Qy 14	Db 18:	Qу 131	Db 17:	0у 13:	•	Qу 12	Db 16:	Оу 12	Db 159	Qy 11,	Db 15:	Оу 108	Db 147	Qy 10:	Db 14:	0у 9(
NISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCE 1 (bases 1 to 162579)	2	Contains ESTs, STSs and GSSs. Contains a novel gene and a novel gene similar to NUP62 (nucleoporin 62kD), complete sequence.	AL390039 162579 bp DNA	ဂ် ယ	892 GAAGCTGTAAAGCTACAGATGGTCTTACAAATGGAACCCCA 1932	.441 gaagotgtaaagotacagatggtottacaaatggaacocca 1481	1832 TTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAAGTTTGTCTCTTCCAGAATT 1891	1381 tractcctctttggaccctgtatctttaacctccttgttaagtttgtctcttccagaatt 1440	1772 CTCAGCCAATGGATGCCCTGGGTTCTCCCCCTTCTTAGGACCTCTAGCAGCTCTAATATTG 1831	1321 ctcagccaatggatgccctgggttctccccttcttaggacctctagcagctctaatattg 1380		61		1201 ggagaagaacgctgttattatgttaatcaatccagaattgtcactgagaaagttaaagaa 1260	1592 CAAAATCGAAGAGTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTA 1651	1141 caaaatcgaagagctttagacttgctaaccgccaaaagagggggaacctgtttattttta 1200	1532 GTCACTGACTCCCTGGTCACCTTGCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCCTT 1591	1081 gtcactgactccctggtcaccttgcaagatcaacttaactccctagcagcagtagtcctt 1140	1472 ACAACCTCTACTACTACTACTACAAACTATCTCAAGAAATAAAT	1021 acaacctctactcagttctactacaaactatctcaagaaataaat		961 cttccttttgttatcagagcaggagtgctaggcagactaggtactggcattggcagtatc 1020	

AUTHORS TITLE JOURNAL

COMMENT

RS Grafam, D.

RS Direct Submission
AL Submitted (19-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Sep 19, 2000 this sequence version replaced gi:9944073.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT: Tr: TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further infor http://www.sanger.ac. Further information rmation can | .uk/HGP/ChrX be at

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //www.chori.org/bacpac/home.htm
                                                                                                                                                                                      /note="L1M4 repeat: 8099. .8419
                                                                                                                                                                                                                                                                                  /note="L1M4 repeat: matches 2857. .3036 of consensus" 6751. .7063
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSq repeat: matches 1. .313 of consensus" 5917. .6014
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/note="7HE1B repeat: matches 1.
10519. .10807
/note="Allsq repeat: matches 3.
11343. .11416
                                                                                         /note="11MC/D repeat: matches 5582. .5648 of consensus" 10039. .10396
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/note="AluSx repeat: matches 1. .312 of consensus"
1457. .2938
/note="LIMEc repeat: matches 356. .1897 of consensus"
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/note="L1PA2 repeat: matches 5329.
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                                                                                                                                                                                                                                                                                                                                                      note="L1PA15 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                  note="49 copies 2 mer ga 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note-"L1PA15 repeat: matches 5325.
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                                                                                                                                                                                                           matches 3036. .4105 of consensus"
                                                                                                                                                             matches 1.
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                                                                   .364 of consensus"
                     . 297
                                                                                                                                                             .306 of consensus"
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17175
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                                                                                                                                                                                                                            /note="HERV17 repeat: 22298. .22742
                                                                                                                                                                                                                                                                                                                                                                        19058. .19492
/note="L2 repeat: matches 2213.
complement(19352. .19843)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L2 repeat: matches 1128. 18706. .18811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17175. .17755

/notc="L2 repeat: matches 1244. .1898 of consensus"

17839. .18106

/notc="MER70A repeat: matches 148. .418 of consensus"

18213. .18318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="37 copies 2 mer tt 67% conserved" 11448. .11983 /note="LIMD3 repeat: matches 7162. .7739 12030. .12337
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2631.
18812. .19057
/note="AluSx repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14808
                                                                                                                                                          /note="AluY repeat: matches 1. .306 of consensus"
23049 .23286
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                                                                                                                                        note="L1MB5 repeat: matches 5403. .5623 of
                                                                                                                                                                                                                                                                                   'note="HERV17 repeat:
                                                                                                                                                                                                                                                                                                                                                       'note-"match: GSS: Em:AQ340313"
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15885. .16086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note-"L1MEc repeat: matches 1309. .1686 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluJb repeat: matches 1. .311 of consensus" [5106. .15492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="LIMEc repeat: matches 1686. .1951 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MER20 repeat:
14255. .14807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1MEc repeat: matches 1951, .2131 of consensus"
|4040, .14254
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13519. .13853
| note="MER7A repeat: matches 1. .346 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3110. .13222
note="FLAM_C repeat: matches 2. .124 of consensus"
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/note="Alusx repeat: matches 1.
12995. .13077 --- matches 103.
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                                                                                        . 23429
                                                                                                                                                                                           "LIMB5 repeat: matches 5623. .6135 of consensus"
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                                                 LIM4 repeat: matches 4019. .4084 of consensus". 24305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMD3 repeat: matches 7162. .7739 of consensus"
12337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches 2688.
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                                 repeat: matches 3097.
                                                                                                   repeat:
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repeat:
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                                                                                                      matches 5006.
 matches 1.
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                                                                                                                                                                                                                                                  matches 4301.
                                                                                                                                                                                                                                                                                   matches 6812.
                                                                                                                                                                                                                                                                                                                      .326
                                 .4043 of consensus"
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26981. .27154
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25437. .25742
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                          Homo sapiens
Eukaryota; Metazoa; Chore
Eukaryota; Metazoa; Primi
Mammalia; Eutheria; Primi
1 (bases 1 to 1629)
Lafont, M. and Perron, H.
Patent: FR 2791140-A 1 2
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/organism="Homo sapiens" /db_xref="taxon:9606"

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Submitted (21-DEC-2000) R&D,
L'Etoile 69280, France
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Viruses; Retroid viruses; Retroviridae.
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 /gene="env"
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/gene="env"
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                                    /clone="pV14"
                                                               /organism="multiple
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                                              /db_xref="taxon:89382"
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CAAAATCGAAGAGCTTTAGACTTGCTAACCGCCAAAAGAGGGGGAACCTGTTTATTTTTA
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Multiple sclerosis retrovirus particles and recombinant envelope trigger an abnormal immune response in vitro, by inducing polyclonal vbeta16 T-lymphocyte activation
Virology 287 (2), 321-332 (2001)
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Birren, B., Linton, L., Nusbaum, C. a Homo sapiens, clone RP11-15N10
Unpublished
2 (bases 1 to 172918)
Birren, B., Linton, L., Nusbaum, C., Anderson, S., Baldwin, J., Barna, N.,
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HTGS_PHASE1; HTGS_DRAFT
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 Nusbaum,C.,
J., Barna,N.,
                                                             Craniata; Ve Catarrhini;
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 Lander, E.,
Beda, F.,
                                           Lander
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                                                                       Vertebrata;
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, Abraham, H., Al
Boguslavkiy, L.,
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                                                                      Euteleostomi;
          Allen, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Mar 2, 2000 this sequence version replaced g All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 2, 2000 this sequence version replaced gi:6970363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project Information Center project name: L3492 Center clone name: 15_N_10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 178000; agarose-fp Insert size: 169718; sum-of-contigs Quality coverage: 2.9 in Q20 bases; Quality coverage: 3.0 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 142569 bases at least Q30 Consensus quality; 156863 bases at least Q30 Consensus quality; 164107 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wl.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ project Information
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14139. .16226
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27725. .30780
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1440 104673	Qy 1381 ttactcotottttggaccotgtatotttaacottcottgttaagtttgtctcttccagaatt
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1320 104553	Qy 1261 attcgagatcgaatacaatgtagagcagaggagcttcaaaacaccgaacgctggggcctc
1260 104493	Qy 1201 ggagaagaacgctgttattatgttaatcaatccagaattgtcactgagaaagttaaagaa
1200 104433	Qy 1141 caaaatcgaagagctttagacttgctaaccgccaaaagagggggaacctgtttatttta
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960 104193	Qy 901 actgaacaagatttatacaatcatgtcgtacctaagccccacaacaaagagtacccatt
900 104133	Qy 841 aatggetetteagaatetatgtgetteeteteattettagtgeeecetatgaceatetae
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780 104013	Qy 721 agcaatactatagacacaaccagctcccaatgcatcaggtgggtaacacctcccacacga
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660 103893	Qy 601 cctgttcctgaacaatggaacaacttcagcacagaaataaacaccacttccgttttagta
600 103833	Qy 541 caaaaccctactaactgttggatgtgcctcccctgcacttcaggccatacatttcaatc
540 103773	Qy 481 catactcgcctggtgagcctatttaataccaccctcactcggctccatgaggtctcagcc

RESULT AX355872 LOCUS

AX355872

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PAT 06-FEB-2002

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AUTHORS
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                                                           CAAGATCAGGCAAGAGAAAAACATGTAAAAGAAGTAATCTCCCAACTCACCCGGGTACAT
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Mammalia; Eutheria;
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TVCWTYETQTGMSDGGGVQDQAREKHVKEVISQSLTRYHGTSSPYKGLDLSKHETLFT
HTRLVSLFNTTLTGLHEVSAQNPTNCWTCLPLNFFPVSIPVPEQWNNFSTEINTTSV
LVGPLVSNLEITHTSNLTCVKFSNTTYTNSQCIFWTNFPTQTVCLPSGIFFVGGTSA
YRCLNGSSESMCFLSFLVPPMTIYTEQDLYNYVISKPRNKRVPILPFVGAGVLGALG
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FLGPLAAIILLLEGPCIFNLLVNFVSSRIEAVKLQMEPKMQSKTKIYRRPLDRPASP
RSDNDDJKGTPDEEISAAQPLLRPNSAGSS"

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RESULT AF208161

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LOCUS DEFINITION

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Drive, Cambridge, MA 02140, USA
Location/Qualifiers
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Sha, M., Lee, X., Li, X., Veldman, G. P., LaVallie, E., Tang, X., Edouard, P.,
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Nature 403 (6771), 785-789 (2000)
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LaVallie,E., Tang,X.Y., Edouard,P.,
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/evidence=not_experimental
2043. .2120
/note="Region: immunosuppresive region"
2335. .3357
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HTRLVSLFNTTLTGLHEYSAQNPTNCWICLPLNFRPYVSIPVPEQWNNFSTEINTTSV
                                                                                                                                                                                                                                                                                                                LVGPLVSNLEITHTSNLTCVKRSNTTYTINSQCIRWTTPPTQIVCLDSGIFFVCGTSA
YRCLNGSSESMCFLSFLPPMTIYTEQDLYNYVISKPRNKRVPILPFVIGAGVLGALG
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2547. .2930

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1869. .1880
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Primates;
                                                                                                 Score 1335.4;
Pred. No. 0;
0; Mismatches
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## Unknown.

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## Lobases 1 to 2946)

## RS Jacobs,K., McCoy,J.M., LaVallie,

## Mcroberg,D., MI,S. and Treacy,M.

## Secreted proteins and polynucleotides enc

## JRNAL Patent: US 6312921-A 3 06-NOV-2001;

## Unclassing unknown  

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Mammalia; Eutheria; Primates; Catarrhini; Ho
1 (bases 1 to 2055)
Perin, J.P., Rieger, F. and Alliel, P.M.
Nucleic sequence and deduced protein sequencendogenous retroviral motifs, and their use;
Patent: WO 9967395-A 22 29-DEC-1999;
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/protein_id="CaC07392.1"
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/translation="PKTANLVADITSLAKYQQVLKTLQGTYP"
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1 (bases 1 to 2599)
2 Perin, J.P., Rieger, F. and Alliel, P.M. Nucleic sequence and deduced protein sequence far endogenous retroviral motifs, and their uses patent: WO 9967395-A 1 29-DEC-1999;
INST NAT SANTE RECH MED (FR): PERIN JEAN PIERRE FRANCOIS (FR); ALLIEL PATRICK M (FR)
                       CAAAACCCTACTAACTGTTGGATATGCCTCCCCCTGAACTTCAGGCCATATGTTTCAATC
                                                                                                                                                              BGCACCTCTAGCCCCTACAAAGGACTAGATCTCTCAAAACTACATGAAACCTCCGTACC
GCACCTCTAGCCCCTACAAAGGACTAGATCTCTCAAAACTACATGAAACCTCCCGTACC
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agcaatactatagacacaaccagctcccaatgcatcaggtgggtaacacctcccacacga
                                                                                                                              GGAGTCACTGTCTGGACTTACTTCACCCAAACTGGTATGTCTGATGGGGGTGGAGTT
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/db_xref="taxon:9606"
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1. .2599
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Catarrhini; Hominidae
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Eukaryota: Metazoa: Chordata: Craniata: Ve Mammalia: Eutheria: Primates: Catarrhini: 1 (bases 1 to 10499)
Perin, J. P., Rieger, F. and Alliel, P. M. Nucleic sequence and deduced protein seque endogenous retroviral motifs, and their us Patent: WO 9967395-A 3 29-DEC-1999;
INST NAT SANTE RECH MED (FR): PERIN JEAN P FRANCOIS (FR): ALLIEL PATRICK M (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                 CAAAATCGAAGAGCTTTAGACTTGCTAACCGCTGAAAGAGGGGGAACCTGTTTATTTTTA
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1. .10499
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                   agcaatactatagacacaaccagctcccaatgcatcaggtgggtaacaccttcccacacga
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                aatggctcttcagaatctatgtgcttcctctctatttttagtgccccctatgaccatctac
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cttccttttgttatcagagcaggagtgctaggcagactaggtactggcattggcagtatc
                                                                              ATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCTCAGCCTATCGTTGTTTG
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Sequence
AX329572
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Patent: WO
Avalon Pha
                                                                                                                                                                                                                 Young, P.E., Augustus, M., Carter, K.C., Ebnorigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic
                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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Pharmaceuticals (US)
Location/Qualifiers
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                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
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                                                                            Score 1333.8;
Pred. No. 0;
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COMMENT
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                                 Submitted (13-NOV-1996)
Genome Sequencing Cente
                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                        Direct Submission
                                                                    Waterston, R.
                                                                                      The sequence of H. sapiens Unpublished (1996)
                                                                                                                                                                                                                               HSAC000064
St. Loui
e-mail:
                                                                                                                          (bases 1 to 56093)
         Department of Genetics, V
St. Louis, MO 63108, USA
                                                                              (bases 1 to 56093)
                                 Sequencing Center
sapiens@watson.wustl.edu
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RG083M05 from
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

SOURCE INFORMATION:

VECTOR: pr Selection: This clone is from the first release of the human BAC library. library contains cloned DNA from a human male fibroblast cell 9785K. For references see: Shizuya et al., Proc. Natl. Acad. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996). рвецо

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Location/Qualifiers
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complement(8186. .8472)
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complement(838..1131)
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complement(7767. .8037)
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kgpellskylgaseqavrdifiraqaakpcilffdefesiaprrghdnygydrvnq
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//gene="WUGSC:H_RG083M05.1" to peroxisome biosynthesis protein PASI (PID:91172019); coded human cDNA C04279 (NID:91467530)"
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(1360, .16971
/gene="WUGSC:H_RG083M05.1"
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/rpt_family="ALU"
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GKDQLFSQPPVLRTASQEGCQELTQEQRDQLRADISIIKGRYRSQSGEDESMNQPGPI
                                                                                                                                                                                                                                13878. .13906
/gene="WUGSC:H_RG083M05.1"
/note="match to human 5' E
                                                                                                                                                                                                                                                                                                                                /gene="WUGSC:H_RG083M05.1"
/note="match to human 5' EST H41382 (NID:917434), bases
143-266"
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/db_xref="GI:1669371"
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/note="match to human fetal brain 5' EST (NID:9970409), bases 1-255, and to human
                                      /rpt_ramily= /
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/note="match to human 5' E
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/note="match to human 3' EST H75782 (NID:g1049794), bases
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_family="L1"
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3' EST R07476
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/gene="WUGSC:H_RG083M05.2"
complement(join(49698...49888,51575...51806))
/gene="WUGSC:H_RG083M05.2"
/gene="WUGSC:H_RG083M05.2"
/note="coded for by human cDNAs W37389 (NID:g1319205),
R65891 (NID:g838529), R65794 (NID:g838432) and R65794
(NID:g838432)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(48406. .48584)
/note="match to human 3' EST N29952 (NID:g1148472), bases
290-455, and 5' EST R12730 (NID:g765806)"
complement(48787. .49405)
/rpt_family="ALU"
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39225
                                                                        /translation="mfyfyfqcgiifcfpqgvyyqigdvvsvideqdgkpyyaqirgf
iqdqyceksaaltwliptlssprdqfdpasyiigpeedlprkmeylefvchapseyfk
srsspfptvptppekcyiwthgptpaitikesvanhl"
                                                                                                                                                                                                                                                                                                                              complement(49674. .49890)

/note="match to human 3' I

EST N29938 (NID:gl148458),

ends of the same clone"
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/rpt_family="ALU"
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complement(38938. .39224)
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pseudogene; region of matches and close matches to
multiple human ESTs, see R68740 (NID:g842257)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="ALU" 21507. .37303
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19550. .19670
                                                      complement(51576.
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129-333"
                                                                                                                                      /protein_id="AAB46345.1"
/db_xref="GI:1669370"
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                    'note="Grail prediction,
                                    /gene="WUGSC:H_RG083M05.2"
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                    score =
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                                                  aatggctcttcagaatctatgtgcttcctcattcttagtgccccctatgaccatctac
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ACTGAACAAGATTTATACAGTTATGTCATATCTAAGCCCCGCAACAAAAGAGTACCCATT
                                        AATGGCTCTTCAGAATCTATGTGCTTCCTCTCATTCTTAGTGCCCCCTATGACCATCTAC
                                                                                 ATAGTCTGCCTACCCTCAGGAATATTTTTTGTCTGTGGTACCTCAGCCTATCGTTGTTTG
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/rpt_family="L1"
55557. .55843
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Waterston, R. H.
Direct Submission
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections of the 
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AG018629 Pan trogl

AG018629 Pan trogl
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Euteleostomi; Homo

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RESULT 2
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Pan troglodytes DNA, clone: PTB-120G11.|
AG113694

AG113694.1 G1:16734213
GSS; GSS (genome survey sequence).
GSS; GSS (male lymphoblast DNA, c.)
Pan troglodytes male 120G11.R.
BAC Library clone:PTB-120G11.R.

Pan troglodytes
                                                                                                                                                                                             atgggagctctgttttcactctatttcactctattaaatcatgcaactgca 875
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               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
     (sites)
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PTB-120G11
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                          1151
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TAATAGAACTGTAACGCTCACCGCATGGCCCAAGATTCCGTTCCTTGGAATCCGTGAGGC
             taatagagctataacactcaccgcatggcccaagattccattccttggtatctgtgaggc 1210
                                                                                                                                                                        atccctttggatccagcagagtgtccactgtgctcctgatccagcgaggtacccattgcc 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiyama, A., Hattori, M. Totoki, Y., Watanabe, H.
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Unpublished
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LIBRARY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="PTB-120G11.R"
/sex="male"
/ce11_type="lymphoblast"
/clone_lib="PTB Chimpanzee
/clone_lib="PTB Chimpanzee
177 c 189 g 144 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pan troglodytes"
/db_xref="taxon:9598"
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86.7%;
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Pred. No. 4.5e-127;
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                 totattgcctgagagcacagcgggaaggacaaggattgggatataaactcagcaattcaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama, A., Hattori, M., To
Totoki, Y., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiyama, A., Hattori, M., Toyoda, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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BAC end sequences of Library PTB
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troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male Library clone:PTB-147IIO.R.
                                                                                                                                                                                                                                                                                                                    160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Site 1
R.Site 2
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing: M13Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tracking errors.
                                                                                                                                                                                                                                                                                                             /clone="PTB-147I10.R"
/sex="male"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/clone_lib= "PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                  35.8%;
89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : pKS145
: SacI
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                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                  Score 475.2; DB 12; Pred. No. 1.9e-125;
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toyoda,A., Taylor,T.D., Yada,T
nd Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taylor, T.D.,
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                                                                                   177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG049953
Pan troglodytes DNA, clone:
AG049953
                                                                                                                                                                                                              and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagqwa 230-0045, Japan (E-mail:chimpbesegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/.Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC enceptions are derived from the chimpanzee BAC library PTB This BAC enceptions.
                                                                                                                                                                                                                                                                                                Submitted (02-AUG-2001) Asao Fujiyama,
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                  Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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GSS; GSS (genome survey
Pan troglodytes male lyn
                                                                                                                                                                                                was generated during the R&D process
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                                                                                   R.Site 1
R.Site 2
                                                                                                                   Vector
                                                                                                                                               Sequencing: -21M13
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/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-030D19.F"
                                                                Location/Qualifiers
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genomic
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TITLE
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                               AUTHORS
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Best Local Similarity
Matches 548; Conserv
                                                                  ORGANISM
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                                                                                                                                                                                                                                                 CTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCATTCCTTGGAATCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAACGGCTACCTTCTTTGGGTCCCCTCCCTTTGTATGAGAGCTCTGT-----T
   Fujiyama,A., Hattori,M., Toyo
Totoki,Y., Watanabe,H. and Sa
BAC end sequences of Library
Unpublished
                                                                        Pan troglodytes DNA, clone: PTB-124K18
AG116971
AG116971. GI:16737490
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-124K18.F.
                                               Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                  Pan troglodytes
                                                                                                                                AG116971
                                       (sites)
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/cell_type="lymphoblast"
/clone_lib="prB Chimpanzee Male
a 185 c 160 g 173 t
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Pred. No. 4.1e-125;
                              Toyoda, A.,
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                     Sakaki,Y.
             PTB
                              Taylor, T.D.,
                                                                                  clone_lib:PTB
                                                        Vertebrata;
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                                                Hominidae;
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                                                                                  Chimpanzee
                                                       Euteleostom1;
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671 gagctcactaaaatgctaatcaggcaaaaacaggaggtaaagcaatagccaatctat 730
ccactcccgatcaggctanaggcttgccattgttcctgcatggctangtgcctgggtttg 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgcctgagagcacagcgggaaggacaaggattgggatataaactcaggcattcaagccag 790
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                                                                               CCGCTCCCGATAGGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAACTGCCCAGGTTCA 495
                                                                                                                                                                                                                                                                                                                        CCATCCCTCCAGATCTGGCAGGGTGTCCACTGTGCTCCTGATCCAGCGAGGCGCCCATTG
                                                                                                                                                                                                                                                                                                                                           ccatccctttggatccagcagagtgtccactgtgctcctgatccagcgaggtacccattg
                                                                                                                                                                                                                                                                                                                                                                                                    GAGCTTTCGCTTGCCATCCACCACTGCTGTTTGCCGCCGCCGCAGACCCGCCTCTGACTT 375
                                                                                                                                                                                                                                                                                                                                                                                                                      gagcttttgttcgccatccaccactgctgtttgccaccgtcacagacccgctgctgactt 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cactctattaaatcatgcaactgca--ctcttctggtccgtgttttttatggctcaagct 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, UKU:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Fujlyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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R.Site 2
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
/clone_lib="154 g 165 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-124K18.F"
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: SacI
: SacI.
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Pred. No. 8e-125;
0; Mismatches 5
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Best Local S
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hes 561;
                          cactctattaaatcatgcaactgcactcttctggtccgtgttttttatggctcaagctga
                                                            tgcctgagagcacagcgggaaggacaaggattggggatataaactcaggcattcaagccag
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             TGCCTGAGAGCACAGTGGGATGGACAATGACCAGGATATAAACCCCAGGCATTCCAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:hhtp://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS; GSS (genome survey sequence). Pan troglodytes male lymphoblast DNA, BAC Library clone:PTB-097K23.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Totoki,Y., Watanabe,H. and Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG096341 710
Pan troglodytes DNA, clone:
AG096341
AG096341.1 GI:16716858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tracking errors.
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                                                                                                                                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
215 c 162 g 165 t
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/db_xref="taxon:9598"
/clone="PTB-097K23.F"
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atanabe,H. a
                                                                                                                                                                                                                             35.3%;
85.1%;
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Pred. No. 7.7e-124;
Pred. No. 7.7e-124;
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nd Sakaki, Y.
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PTB-097K23.F,
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                                                                                                                                                                                                                                        Length 710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        642 TCTTGGAAGCAGCCTGCCACCATCTTGGAAGCTCTATGAGCAAGGACCCCCCAGTAACA
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                                                                                                                                                                                                                                                                                                                                      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sgc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC enwas generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AG072852.1 GI:16624654
GSS; GSS (genome survey
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Pan troglodytes DNA, clone:
AG072852
                                                                                                                                                                                                                                                                                                                        was generated during the clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC end sequences of Library
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Totoki, Y., Watanabe, H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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        152
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R.Site 2
                                                                                                                                                                                                                                                                              Sequencing: M13Rev
                                                                                                                                                                                                                                             Vector
        ρ
/clone="PTB-064H14.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
190 c 157 g 170 t
                                                                                                              /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                             location/Qualifiers
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nd Sakaki, Y.
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PTB-064H14.R,
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              Fujlyama, A., Hattori, M., Totoki, Y., Watanabe, H. a
                                                        Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                         Pan troglodytes DNA, clone: PTB-102B0; AG099717.
AG099717.1 GI:16720234
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, BAC Library clone: PTB-102B07.F.
Pan troglodytes
                                               Unpublished
                                                                                                    Pan troglodytes
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                    (bases 1 to 712)
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                and
                Toyoda, A.,
nd Sakaki, Y
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Catarrhini;
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                         Taylor, T.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
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/clone_lib="PTB Chimpanzee
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/db_xref="taxon:9598"
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Pred. No. 1.2e-119;
D; Mismatches 66;
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TCGTCGGCCAACCTCCCCAATGGCACTTGGGTTTTCCTGTTGAGAGGGGGGGACTGAGAGA
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                                                                                                                                                                                                                                                                                                                      507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          689 bp DNA Pan troglodytes DNA, clone: PTB-130M15.F, AG121669 GSS: GSC /~~~~
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Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-130M15.F.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
159 c 176 g 189 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="PTB-130M15.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Pan troglodytes"
/db_xref="taxon:9598"
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Class: shotgun
High quality sequence start: 40
High quality sequence stop: 567
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 921)
1 (bases 1 to 921)
1 (control of clone end sequences from Ent
HM1:HMS: sheared DNA library (2001)
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Dr., Tel: 301 838 0208 Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Brendan J Loftus
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                             method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999).
                                                                                                                                                                    /Clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: BSt I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
                                                                                                                                                                                                                                                                                     /db_xref="taxon:5759"
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Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japa
                                                                                                                                                        AG076758
Pan troglodytes DNA, clone: PTB-071A23.R, genomic su AG076758
AG076758.1 GI:16628560
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB
BAC Library clone:PTB-071A23.R.
Pan troglodytes
                                            Fujlyama, A., Hattor1, M.,
Totok1, Y., Watanabe, H. a
                                                                                                   Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                             Unpublished
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Primates;
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                                                                              59
AG102951
Pan troglodytes
AG102951
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Query Match
Best Local Similarity
Matches 480; Conserv
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                                                                                                   gaccgcatccatctttaaacatggggcttgcaacttagctcacacccgaccaatcagaga
                                                                                                                                                                                agacaggactagctggatttcctaggctgactaagaatcccnaagcctanctgggaaggt 612
                                                                                                                                                                                                                                                                   cagttgtcagccaacctccccaacagtacttgggttttcctgttgagagggtggactgag
                                                                                                                                                                                                                                                                                                                                                                                                      gatgccctggactctcccccttcttaggacctctagcagctataatattttttactcctctt 252
                                      gctcactaaaatgcta
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                                                                                                                                                                 AGACAGGACTAGCTGGATTTCCTAGACCGACTAAGAATCCCTAAGCCTAGCTGGGAAGGT
                                                                                                                                                                                                                                             CGGTCGTCAGTCAACCTCCCCAGCAGCACTTGGGTTTTCCTGTTGAGAGGGGGGTACTGAG
                                                                                                                                                                                                                                                                                                                              TGAGGAAATCTCAACTGCACAACCCCTACCATGCCCCATTTCAGCAGGAAGCAGGTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tggaccctgtatcttcaacttccttgttaagtttgtctctttccagaattgaagctgtaaa 312
GCTCTCGAGCATGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
157 c 187 g 171 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-071A23.R"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.8%;
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: SacI
: SacI.
44
                                        889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 435.6; DB 12;
Pred. No. 4.6e-114;
0; Mismatches 76;
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DNA,

clone:

3 bp DNA PTB-106G16.F,

genomic

GSS 03-NOV-2001 survey sequence.

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REFERENCE
AUTHORS
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AUTHORS
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KEYWORDS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                ctgagcttttgttcgccatccaccactgctg-tttgccaccgtcacagacccgctgctga
                                                                                     atttcactctattaaatcatgcaactgcactcttctggtccgtgttttttatggctcaag
                                                                                                                                                                                                                            ctattgcctgagagcacagcgggaaggacaaggattgggatataaactcaggcattcaag
                                                                                                                                                                                                                                                                                               cagagagctcactaaaatgctaatcaggcaaaaacaggaggtaaagcaatagccaatcat 726
                                                                                                                                                          ccagcaacagcaacccctttgggtcccctcccattgtatgggagctctgttttcactct
                                                                                                                                                                                                             CTATTGCCTGAGAGCACAGCGGGAGGGACAAGGATCGGGGATATAAACCCAGGCATTTGAG
                                                                                                                                                                                                                                                                               CAGAGAGCTCACTAAAATGCTAATTAGGCAAAAACAGGA-GTAAAGAAACAGCCAATCAT
CTGAGCTTTCACTTGCTGTCCACCACTGCTGTTTTGTTGCCATTGCAGACCCACCGCTGA
                                                                   ATTTCACTCTATTAAATCTTGCAACTGTGCTCTTCTGGTCCGTGTTTGTAATGGCTCAAG
                                                                                                                                        CCGGCAACGGCAACCCCCTTTGGGTCCCCTCC--TTGTATGGGAACTCTGTTTTCACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC encaps generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG102951.1 GI:16723468
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-106G16.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162
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R.Site 1 : SacI
R.Site 2 : SacI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
186 c 167 g 167 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-106G16.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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nd Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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KEYWORDS
SOURCE
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AQ381711
LOCUS
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                647
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                                            22
gaatcccnaagcctanctgggaaggtgaccgcatccatctttaaacatggggcttgcaac 646
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                                            GAATTCCTAAACCTAGCTGAGAAGGTGACCGCATCCACCTTTAAACACGGGGCTTGCAAC
                                                                                                       517;
                                                                                                                                                                                                                                                                                                                                                                                   Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq_primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Other_GSSs: RPCI11-165G20.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao, S., Adams, M.D., Nierman, W., Malek, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 611)
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RPCI11-165G20.TJ RPCI-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Map Building
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence.
                                                                                                                   Similarity
                                                                                                                                                                                               152
                                                                                                       Conservative
                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:753139"
/db_xref="taxon:9606"
/clone="RPCI-11-165G20"
/clone_lib="RPCI-11"
                                                                                                                                                                                     /sex="Male" /Jex="Male" /Jex="Male" /Jex="Vector: pBACe3.6; Site_1: /note="Vector: pBACe3.6; Site_1: RPCI11 Human Male BAC Library" 150 c 135 g 154 t
                                                                                                                                                                                                                                                                                                                                              1. .61
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                     /sex="Male"
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                                                                                                                  32.4%;
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Primates;
                                                                                                    Score 430.6; DB
Pred. No. 1.2e-11
D; Mismatches 6
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-agagagctcactaaaatgctaatcaggcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      đđ
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                                                                                                    DB 12;
2e-112;
3 62;
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                                                                                                                                   611;
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RPCI-11-165G20,
                                                                                                     21;
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                                                                                                                                                                                    Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
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Pan trogl
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                       Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                             Sequencing: M13Rev
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troglodytes male lymphoblast DNA, clone_lib:PTB
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Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K. Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C
                                                                             Homo sapiens
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
/ 192 c 199 g 170 t 5 others
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/clone="PTB-084E11.R"
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Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
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CCATTGTTCCTGCACAGCTAAGTGCCTGGGTTCATCCTAATCAGGCTGAACACTGTTCGC
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Class: BAC ends.
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Unpublished (1998
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
211 c 154 g 166 t
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1. .714
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/clone="RPCI-11-64L19"
/clone_lib="RPCI-11"
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/db_xref="GDB:7524474"
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Pred. No. 9.4e-112;
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Perfect score:
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Match
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         June 20, 2002, 09:38:01; Search time (without 3341.320
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                                                                                                                                                                                                                                                                   APPLICANT: Nurberg, David
APPLICANT: Merberg, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Evans, Cheryl
APPLICANT: Spaulding, Vilki
TITLE OF INVENTION: SECRETED PR
TITLE OF SECUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                CURRENT APPLICATION DATA:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
APPLICATION NUMBER: FILING DATE:
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RESULT 3
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SEQUENCE CHARACTERISTICS:
LENGTH: 279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: BIOWN, SCOTT A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Applic Patent No. 5786465
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                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                        STREET: 87 CambridgePa CITY: Cambridge STATE: Massachusetts COUNTRY: U.S.A. 2IP: 02140
                                                                                                                                                                                                                                                                                 APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED
TITLE OF INVENTION: ENCODING
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
                               APPLICATION NUMBER:
                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cagcaaccccctttgggtcccctcccattgtatgggagctctgttttcactctatttcac 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctcactaaaatgctaatcaggcaaaaacaggaggtaaagcaatagccaatcatctattgc 733
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Similarity 85.1%;
               DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08721489
                                                                                                                                                                                                                87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                   McCoy, John
Lavallie, Edward
Racie, Lisa
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                                                                                                                                                                                                                                     Genetics Institute,
                               US/08/721,489
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Pred. No. 2.4e-61;
1; Mismatches 38
                                                                                                                                                                                                                                                                                      THEM
                                                                                                                                                                                                                                                                                                    PROTEINS AND POLYNUCLEOTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 58, Application US/08691563C
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                APPLICANT:
                      SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,56:
                                                                                                                                                                                                                                APPLICANT: Florence KOMURIAN-PRADEL
APPLICANT: Colette JOLIVET
APPLICANT: Bernard MANDRAND
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT
TITLE OF INVENTION: THERAPEUTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION
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                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                    STREET: 700 Sources CITY: Alexandria
                                                                                                                        COUNTRY: U
ZIP: 22314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 NTCANTAAAATGATNATTNGGCAAAAACAGGAGGTAAAGAAATAGCCAATCATCTATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
            FILING DATE:
                                                                                                                                                 STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                     6001987
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Frederic BEDIN
Glaucia PARANHOS-BACCALA
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               02-AUG-1996
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85.1%;
                           US/08/691,563C
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Pred. No. 2.4e-61;
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                                                      Version #1.30
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US-08-691-563C-46
US-08-691-563C-46
; Sequence 46, Application US/08691563C
; Patent No. 6001987
; Patent No. 6001987
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                        APPLICANT:
APPLICANT:
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APPLICANT:
            APPLICANT:
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les 333; Conserv
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          Frederic BESEME
Frederic BEDIN
Glaucia PARANHOS-BACCALA
Florence KOMURIAN-PRADEL
Colette JOLIVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1722 base pairs
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                                                                             Herve PERRON
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Bernard MANDRAND
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TELEPHONE: 703-836-6400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atttgagatcgaatataatgtagagcaggaggaccttcaaaacactgcaccctgggggcctc
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AGTAGCTAGAGCGGTCATCGGCCAA-ATTCCCAACAGCAGTTGGGGGTGTCCTGTTTAGAG
                                                                                                                                         gtcacccctcccgaggaaatctcaactgcacaacccctactacactccaattcagtagga 481
                                                                                                                                                                                                                    TTCTACCAAGGACCCCTGGAACGATCCACTGGCACTTCCACT---
                                                                                                                                                                                                                                        atctaccgtggacccctggaccggcctgctagactatgctctgatgttaatgacattgaa 421
                                                                                                                                                                                                                                                                                                                                                          gaagctgtaaaagctacaaatagttcttcaaatggaaccccagatgcagtccatgactaaa 361
                                                                                                                                                                                                                                                                                                                                                                                                                                             TTACTCACCTTTGGGCCCTGTATTTTTAAGCTTCTTGTCAAATTTGTTTCCTCTAGGATC
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                         agcagttagagcagttgtcagccaacctccccaacagtacttgggttttcctgttgagag
                                                                                                          GATTCCCCTCTGGAAGACACTACAACTGCAGGGCCCCTTCTTTGCCCCCTATCCAGCAGGA
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Pred. No. 2e-46;
0; Mismatches 2
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TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 1859 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-691-563C-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                          1491
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                                                                                                                                                                                                                                                                                 1371
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FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,02
                                                                                              1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Oliff & Berridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
 482 agcagttagagcagttgtcagccaacctccccaacagtacttgggttttcctgttgagag 541
                                                                                                                           362
                                                                                                                                                                                       302
                                                                                                                                                                                                                                                                                                              182
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STATE: Virginia
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                                                                                                                                                                                                                  CAAAACCGTCAAGGCCTAGACCTCCTCACTGCTGAGAAAGGAGGACTCTGCACCTTCTTA 1256
                                                                                                                                                                                                                                                                              gtcacccctcccgaggaaatctcaactgcacaacccctactactacactccaattcagtagga 481
                                                                                              TTCTACTGAGGACCCCTAGACCCAACCCCCTGGCCCTTTCACTGGCCTAAAGAGTT-----
                                                                                                             GAGGCCATCAAGCTACAGATGGTCTTACAAATGGAACCCCAAATGAGCTCAACTATCAAC 1550
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                                 · CCCCTCTGGAGGACACTACCACTGCAGGGCCCCATCTTTGCCCCCTATCCAGAAGGA
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ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLAC:
THERAPEUTIC PURPOSES
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; ORGANISM: Nucleotide sequence US-09-078-294-4
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CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 80246
TYPE: DNA
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Best Local Similarity
Matches 360; Conserv
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APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
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Pred. No. 7.2e-44;
0; Mismatches 234
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; ORGANISM: Nucleotide sequence of HC-contig
US-09-078-294-3
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Best Local Similarity
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CURRENT FILLING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 1.9e-40;
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Best Local
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INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: VACCINE COMPRISING FOWLPOX VIRUS
TITLE OF INVENTION: RECOMBINANTS EXPRESSING THE ENVE:
TITLE OF INVENTION: AVIAN RETICULOENDOTHELIOSIS RETRU
                                                                                                                  1507
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
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NAME: MURPHY JR., GERALD M.
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CORRESPONDENCE ADDRESS:
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APPLICANT:
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                                                1567 TTGAACGGCTTCCTTCCATATTTGCTACCCTTGTTAGGCCCCCTGTTTGGGCTCATATTG
                                                                                                                                                                                                                                                                                                                   thes 167;
242 ttactcctctttggaccctgtatcttcaacttccttgttaagtttgtctctttccagaatt
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REFERENCE/DOCKET NUMBER: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 199301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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CITY: Falls Church
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                                                                                                                                     atttgagatcgaatataatgtagagcagaggaccttcaaaacactgcaccctggggcctc
                                                                                                                  CTCCAAGAGGACCTTATCGAGAGAAAACGTGCACTGTACGACAACCCCCTGTGGAGCGGC
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CALVERT, JAY G.
WITTER, RICHARD L.
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53.7%;
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TTCCTGACCCTCGGCCCGTGCATTATGAAGACCCTGACTCGCATTATACATGACAAAATT 1686

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RESULT 10
US-09-011-745-8
; Sequence 8, Application US/09011745
; Patent No. 6165715
; GENERAL INFORMATION:
; APPLICANT: COllins, Mary KL
; APPLICANT: Weiss, Robin A
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, NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: n is any nucleotide
US-09-011-745-1
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US-09-011-745-1
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CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Collins, Mary KL
APPLICANT: Weiss, Robin A
APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER OF SEQ ID NOS: 29
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APPLICANT: Takeuchi, Yasuhiro
APPLICANT: Cosset, Francois-Loic
TITLE OF INVENTION: Expression systems
FILE REFERENCE: 09/011,745
CURRENT FILING DATE: 1998-06-22
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER APPLICATION NUMBER: PCT/GB96/02061
EARLIER FILING DATE: 1996-08-23
EARLIER APPLICATION NUMBER: GB9517263.1
EARLIER FILING DATE: 1995-08-23
NUMBER: OF SEO ID NOS: 29
SOFTWARE: PATENTIN Ver. 2.0
SEO ID NO 8
LENGTH: 5865
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; LOCATION: (3802)
; OTHER INFORMATION: n is
US-09-011-745-8
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Best Local Similarity
Matches 167; Conserv
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LOCATION: (3614)
OTHER INFORMATION: n is
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LOCATION: (3613)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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NAME/KEY: misc_feature
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ctcagccaatggatgccctggactctccccttcttaggacctctagcagctataatattt 241
                                                                          atttgagatcgaatataatgtagagcagaggaccttcaaaacactgcaccctgggggcctc 181
                                                     caagaaaaatgctgtttttatgctaacaagtcaggaattgtgagaaacaaaataagaacc 2907
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Pred. No. 8.3e-17;
0; Mismatches 144;
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                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                              1026
                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
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APPLICANT:
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                               PRIOR APPLICATION DATA:
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CITY: Alexandria
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                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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ttcactctattaaatcatgcaactgcactcttctggtccgtgttttttatggctcaagct 908
                                                          agcaacagcaaccccctttgggtcccctcccattgtatgggagctctgttttcactctat 848
                                                                                             4, Application US/08232463
5670367
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                                                                                                                                                                                                                                                                                                                                                                                            (703)683-4109
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                                                                                                                                                         Conservative
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SYSTEM: PC-DOS/MS-DOS
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US-08-766-528-1
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                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
                                                                                                                                                                                                                                               TELEFAX: (617)227-594
INFORMATION FOR SEQ ID NO:
 1619
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: MG TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Louis Myers
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                           NAME: Louis Myers REGISTRATION NUMBER: 35,965
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(617)227-5941
                                                             Conservative
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55.7%;
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                                                                           Score 50.8; DB 4; Pred. No. 1.7e-06;
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RESULT 14
US-08-258-420-8
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US-08-766-528-3
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Best Local :
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 8132 base pairs
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APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                    7273 CTTAGAGAAAGGTTGGAGAAGCGTCGAAGGGAAAAGGAAACTACTCAAGGGTGG
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REFERENCE/DOCKET NUMBER: MG
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Pred. No. 6e-06;
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US-08-258-420-8
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Query Match
Best Local Similarity
Matches 177; Conserv
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INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
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SOFTWARE: WORDPERfect 5.1
CURRENT APPLICATION DATA:
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LENGTH: 1911 bases
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                    1588 AAAGAAGAATGTTGTTTTATGCAGACCACACGGGGCTAGTGAGAGACAGCATGGCCAAA 1647
                                                                                                                                                                                                                                                                                                                                                                                                                    1528 CAGAACCGCAGAGGCCTAGATTTGCTATTCCTAAAGGAGGGGAGGTCTCTGCGCAGCCCTA 1587
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STATE: New Jersey
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GTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCAACAATATCACCAGCTG
                                                                                  ATAGTACTCTTACTGATCTTACTCTTTGGACCTTGCATTCTCAATCGATTAGTCCAATTT
                                                                                                   gcagctataatatttttactcctcttttggaccctgtatcttccaacttccttgttaagttt 286
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Pred. No. 2.1e-05;
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; TOPOLOGY: linear
; MOLECULE TYPE: genomic
US-08-258-420-9
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US-08-258-420-9
; Sequence 9, Application US/08258420
; Patent No. 5710037
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.5%;
Best Local Similarity 48.1%;
Matches 177; Conservative
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OPERATING SYSTEM: MS-DOS
SOFTMARE: WORDERT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,420
FILING DATE: 10-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER:
FILING DATE:
FILING DATE:
FILING DATE:
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NAME: Olstein, Elliot M.
REGISTRATION UMBER: 24,025
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
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CTATE: New Jersey
rrqA
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                                                                                                                                                                                   1702 TTAAGAGAAAGGCTTAATCAGAGACAAAAACTATTTGAGACAGGCCAAGGATGGTTCGAA 1761
                                                                                                                                                                                                                                                           1642 AAAGAAGAATGTTGTTTTTATGCAGACCACACGGGGCTAGTGAGAGACAGCATGGCCAAA 1701
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LENGTH: 1965 bases
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                                                                                                            1762 GGGCTGTTTAATAGATCCCCCTGGTTTACCACCTTAATCTCCACCATCATGGGACCTCTA 1821
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MEDIUM TYPE: 3.5 inc
                                                                                                                                                      179
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287 gtctcttccagaattgaagctgtaaagctacaaatagttcttcaaatggaaccccagatg 346
                                                                                                                                                                                                                                                                                62 ggggaagaatgctgttagtatgttaatccaatctggaatcattactgagaaagttaaagaa 121
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ZIP: 07068
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                                                             6 Becker Farm
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Becker Farm Road
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Pred. No. 2.1e-05;
0; Mismatches 176;
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Db 1882 GTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTGACTCAACAATATCACCAGCTG 1941
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Qy 347 cagtccat 354

Db 1942 AAGCCTAT 1949

Search completed: June 20, 2002, 09:40:25 Job time: 8535 sec

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Result
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Maximum DB seq length: 2000000000
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| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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Clone 5M6 from MSR
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Human diagnostic a
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cc polypeptide (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The polymerased sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques cc to restore normal activity of (II) is useful in generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess blodiversity amino acid sequences. AAS64197-AAS94564 represent novel human cc and coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed cate intront of the printed code in the printed of the company of the printed code in the p
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24-FEB-2000;
24-FEB-2000;
12-MAY-2000;
                                                                                                                                                                                                                      its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies against DITHPs and in assays to identify modulators of DITHP expression and activity. The anti-DITHP antibodies and antagonists may also be used to down regulate expression and activity. The anti-DITHP antibodies and antagonists may also be used as diagnostic agents for detecting the presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAS30986-AAS31196 represent human diagnostic and therapeutic (DITHP) polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II) which include e.g. enzymes, and proteins involved in growth and development and receptors (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide expression by rectifying mutations or deletions in a patient's genome, that affect the activity of the DITHPs, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder, Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma, leukaemia, autoimmune disorders, and respiratory disorders. Additionally, (I) may be used to produce the DITHPs, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) and the complementary exercises are also be used as DNA morboe in dispersion to the protein of the cell to express the protein. (I) and the complementary exercises are also be used as DNA morboe in dispersion to the complementary exercises are also be used as DNA morboe in dispersion to the cell to express the protein. (I) and the complementary exercises are also be used as DNA morboe in dispersion to the complementary exercises are also be used as DNA morboe in dispersion to the cell to express the protein.
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gaagctgtaaaactactaattgttcttcaaaaggagccccagatgcagtccatgactaag
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                                                                           Score 778.8; DB 22;
Pred. No. 6.7e-245;
0; Mismatches 112;
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Best Local (
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       1200
                                                1140
                                                                                                                                                                                                                                                                                                                         Nucleotide fragment of retrovirus (MSRV) used biological sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyA_signal
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                                                                                                                                                 Sequence 2030 BP; 574 A; 559 C;
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                                                                                                                                                                                                                                                                      present sequence represents the nucleotide sequence corresponding the 3' env region and long terminal repeat sequences from clone
    2000-506097/45
                                                           tcaaaatcgaagagctttagacttgctaaccgccaaaagagggggaacctgtttatttt 60
                                              tcaaaatcgaagagctttagacttgctaaccgccaaaagagggggaacctgtttattttt 1199
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                                                                                          Conservative
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presence of MSRV-1 retrovirus
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Secreted protein; testes; brain; blood; placenta; human; murine; thymus; bone marrow; treatment; prevention; nutrition; cytokine; immune; vaccine; cell proliferation; cell differentiation; suppressor; tumour inhibition; haematopoiesis regulator; activin; inhibin; chemotractic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; tumour; cadherin; tumour invasion suppressor; gene therapy; tissue growth; ss.

Human secreted

protein AJ172_2

CDNA.

Homo

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21-NOV-1997;
18-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel human secreted proteins encoded by polynucleotides isolated from human adult testes, adult brain, adult blood or adult placenta, or murine adult bone marrow or thymus cDNA libraries. The products of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful
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The invention relates to isolated polynucleotide (I) and C polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful in generating antibodies against it, detecting or GC (II), (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO or after viron intromby high and not appear in the printed CC and to refer the content of the printed of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, used diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and trains and trains are specific trains.
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23-AUG-2000; 2000US-0649167
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food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                                                                                                              retrovirus (HERY) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulin- dependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility.
                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid sequences from human endogenous retrovirus-W expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnand
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dependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility.
                                                                                                                                                                                                                                                      This sequence represents clone cl.C4C5 of the human endogenous retreated with the first sequence. The nucleic acids, their fragments or peptides or HERV) W genome. The nucleic acids, their fragments or peptides or by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid sequences from human endogenous retrovirus-W - expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnancy
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                                                                                                                                                                           The present sequence represents an endogenetic retroviral nucleic acid fragment, which is associated with an autoimmune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autoimmune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autoimmune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to
                                                                                                                                                                                                                                                                                       Disclosure; Page 46; 53pp; French.
                                                                                                                                                                                                                                                                                                            New nucleic acid from human endogenous retrovirus, useful e.g. diagnosis of autoimmune disease and complications of pregnancy contains at least part of the gag gene
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Clone; human endogenous retrovirus; genome; autoimmune disease; multiple sclerosis; rheumatoid polyarthritis; insulin-dependent diabetes; disseminated lupus erythematosus; pregnancy; chromosomal marker; ss.
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Matches 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents clone cl.PH74 of the human endogenous retrovirus (HERV) W genome. The nucleic acids, their fragments or peptides encoded by them are markers of autoimmune disease (e.g. multiple sclerosis, rheumatoid polyarthritis, disseminated lupus erythematosus, insulindependent diabetes and related pathologies) and of abnormal or unsuccessful pregnancy and can be used as chromosomal markers for susceptibility to these conditions, or proximity markers of genes associated with this susceptibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequences from human endogenous retrovirus-W expressed exclusively in placenta and useful in diagnosis and therapy of autoimmune disease, and abnormal or failed pregnance.
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Query Match Best Local S Matches 782

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                 The present sequence represents an endogenetic retroviral nucleic acid fragment, which is associated with an autolimnune disease, and is integrated into the human genome. The fragment is originally derived from a novel retrovirus, human endogenous retrovirus W (HERV-W). The HERV-W retrovirus is associated with autolimnune disease, failure of pregnancy or disorders of pregnancy. The nucleic acid fragment, or proteins derived from it, are useful for diagnosis of autolimnune disease (specifically multiple sclerosis) and for monitoring pregnancy. The nucleic acid fragments may also be used for in situ labelling of isolated chromosomes, while the transcription product can be used to study or monitor T cell proliferation in vitro.
                                                                                                                                                                                      New nucleic acid from hudiagnosis of autoimmune contains at least part of
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Ott,C. and Bedin,F.
RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN PARTICULAR ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIXAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC USES
PATENT: WO 9902666-A 12 21-JAN-1999;
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of H_RG083M05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEIGHBORING SEQUENCE INFORMATION:
The orientation of this clone is unknown.
clone is at base position 1 of H_RG083M05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission Submitted (13-NOV-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           confirmed by restriction digest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Genetics, Washington St. Louis, MO 63108, USA e-mail: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone
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complement(4948.
/rpt_family="ALU"
complement(6581.
                                                                                                                                                                   /protein_id="AAB46346.1"
/db_xref="GI:1669371"
                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="7"
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                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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RG083M05
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This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping once, or longer because we provide a small overlap between between

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was

This clone is from the first release of the human BAC library. library contains cloned DNA from a human male fibroblast cell i 9785K. For references see: Shauya et al., Proc. Natl. Acad. 89:8794-8797 (1992); Kim et al., Genomics 34:213-218 (1996). Actual start of this actual end is at 560 line

at 56093

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KTRLALSQSHLMTALGHTRPSISEDDWKNFAEL"

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complement(15618.
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/note="match to multiple human ESTs, see N81064
(NID:g1243765), H48897 (NID:g988737), and M78831
(NID:g273146)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13670. .13793
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143-266"
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complement(8186. .
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/rpt_family="ALU"
                                                                                                                                                                                                              complement (40247. /rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                       /note="Grail prediction, score /evidence=not_experimental complement(38938 . 39224) /rpt_family="ALU"
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/rpt_family="ALU"
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complement (47027.
                                                                                       complement(45614 ..457
/note="match to human
                                                                                                                      complement(45474.
/rpt_family="ALU"
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/rpt_family="ALU"
                                                                                                                                                                                                                                                                       NID:g1148633)"
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21-348"
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/note="match to human 5' E
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/note="match to human 3' E
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                                                                                       H48898 (NID:g988738),
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3' EST
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Best Local Similarity
Matches 1133; Conserv
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                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                61 aggggaagaatgctgttagtatgttaatcaatctggaatcattactgagaaagttaaaga 120
                                                                                                                                                                                                                                                                                                                                                                     1 tcaaaatcgaagagctttagacttgctaaccgccaaaagagggggaacctgtttattttt 60
                                                                 aatttgagatcgaatataatgtagagcagaggaccttcaaaacactgcaccctggggcct 180
                  tgaagctgtaaagctacaaatagttcttcaaatggaaccccagatgcagtccatgactaa
                                                                                                                                                                                                          AATTCGAGATCGAATACAACGTAGAGCAGGAGGTTCGAAACACTGGACCCTGGGGCCT
                                                                                                                                                                                                                                                                               AGGGGAAGAATGCTGTTATTATGTTAATCAATCCGGAATCGTCACTGAGAAAGTTAAAGA
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complement(47365.47782)
/note="match to multiple h
(NID:g1319089)"
47898.48115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match to human 3', EST N29952 (NID:g1148472) and EST N29938 (NID:g1148488), sequences are from opposite ends of the same clone" complement(49698. 51806)
/gene="MUGSC:H_R0083M05.2" complement(join(49698. 49888,51575. .51806))
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/note="coded for by human cDNAs W37389 (NID:g1319205), R65891 (NID:g838529), R65794 (NID:g838432) and R65794 (NID:g838432)
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290-455, and 5' EST R12730 (NID:g765806)"
complement(48787. .49405)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="L1" 55557. .55843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Grail prediction, score =
/evidence=not_experimental
complement(52052. .52329)
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/note="match to human 3'
309-440"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="WUGSC:H_RG083M05.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     77.98;
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1035.2; DB 9; Pred. No. 6.1e-304; 0; Mismatches 111;
-CAAATGGAGCCCAAGATGCAGTCCAAGACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .49672)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTS,
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 56093;
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Web site.http://www.news.com/wigsc
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Waterston P u
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6 (bases 1 to 149194)
Waterston, R.H.
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University School of Me
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: submissions@watson.wustl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
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                                                                                                CCACAGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGGTTCCATTCCTT-GAA
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                                                                                                                                                                        ACCCATTGCCGCTCCCAATCGGGCTAAAGGCTTGCCATTGTTCCTGCATGGCTAAGTGCC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1049)
Perin,J.P., Rieger,F. and Alliel,P.M.
Nucleic sequence and deduced protein sequence family endogenous retroviral mottifs, and their uses Patent: WO 9967995-A 3 29-DEC-1999;
INST WAT SANTE RECH MED (FR); PERIN JEAN PIERRE (FR) FRANCOIS (FR); ALLIEL PATRICK M (FR)
                                                                                                                                                                                                           Hominidae;
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                                      (FR);
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1 tcaaaatcgaagagctttagacttgctaaccgccaaaagagggggaacctgtttattttt Score 1023.2; DB 6; Pred. No. 2.7e-300; 0; Mismatches 111; Indels Length 10499; 14; Gaps 60 ω ••

tgaagctgtaaagctacaaatagttcttcaaatggaaccccagatgcagtccatgactaa GCTACTCCTCTTTGGACCCTGTATCTTTAACCTCCTTGTTAACTTTGTCTCTTCCAGAAT tttactcctctttggaccctgtatcttccaacttccttgttaagtttgtctcttccagaat 9317 9365 360 300

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aatctaccgtggacccctggaccggcctgctagactatgctctgatgttaatgacattga GATCTACCGCAGACCCCTGGACCGGCCTGCTAGCCCACGATCTGATGTTAATGACATCAA 420 9425

agtcacccctcccgaggaaatctcaactgcacaacccctactacactccaattcagtagg 9485 480

AAGCAGTTAGAGC-GGTCTCGGCCAACCTCCCCAACAGCACTTAGGTTTTCCTGTTGAGA aagcagttagagcagttgtcagccaacctccccaacagtacttgggttttcctgttgaga 9544 540

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Martin, R.,
  Martindale, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (30-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced g1:12083977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'vorking draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
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Sequencing vector: M13; L08821

Chemistry: Dye-primer Bodipy: 2% of reads

Chemistry: Dye-terminator B1g Dye: 98% of reads

Chemistry: Dye-terminator B1g Dye: 98% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 186874 bases at least Q40

Consensus quality: 189446 bases at least Q30

Consensus quality: 190585 bases at least Q20

Estimated insert size: 189222; sum-of-contigs estimation

Quality coverage: 8.2x in Q20 bases; sum-of-contigs estimation
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61734
133018
133118
164867
164967
180053
180153
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Center clone name: RP11-533J15
----- Summary Statistics
Sequencing vector: plasmid; M77789
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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       ø
                                         /clone="RP11-533J15"
                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                         1. .188919
                                                                                                                                                                                                                               Location,
                                                                           /chromosome="12"
                                                                                                                                                                                                                                                         61633: contig of 61633 bp in length
61733: gap of unknown length
133017: contig of 71284 bp in length
133117: gap of unknown length
164866: contig of 31749 bp in length
164966: gap of unknown length
180952: contig of 15086 bp in length
180152: gap of unknown length
180152: gap of unknown length
188919: contig of 8767 bp in length.
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                                                                                                                                                                                                  caatagccaatcatctattgcctgagagcacagcgggaaggacaaggattgggatataaa
                                                                                                                                                                                                                                                GGGCACCCCTCCTGAGGAAATCTCAACTGCACAACCCCTACTATGCCCCAGTTCAGCAGG
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             agacccgctgctgacttccatccctttggatccagcagagtgtccactgtgctcctgatc 1011
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 AGACCCGCCACTGACTTCCATTCCTCTGGGTCCGGCAGGGTGTCCGCTGTGCTCCTGATC
                                            ACCAATCAGGTAGTAAAGACAGCTCAGTAAAAAGCTAGTTTGGCAAAAACAGGAGGTAAAG
                                                                                                                                                                                                                                                                                  AGCTGGGAAGGTGATCACATCCACCTTTAAACATGGGGCTTGCAACTTAGCTCACACCCG
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86.7%;
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COMMENT

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Institute/ MIT Center

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Research

Center: Whitehead

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RESULT 8
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TITLE
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                                                                                JOURNAL
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                                                                                                                            Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Travis, N., Travis, N., Trigillo, J.,
Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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l (bases 1 to 161571)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-141A18
Unpublished
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC092708
Homo sapiens chromosome 18 clone SEQUENCE, 3 unordered pieces.
Submitted (20-JUL-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT;
                                                                                                          Direct Submission
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32931 33030: gap of 100 bp
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Location/Qualifiers
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Insert size: 161371; sum-of-contigs
Quality coverage: 9.8 in Q20 bases; agarose-fp
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Sequencing vector: Plasmid: n/a; 100% of read
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Assembly program: Phrap; version 0.960731
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Consensus quality: 161352 bases at least Q20
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CCATTTTGGAAGTGGCCTGCCGTCTTGGGAGC
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RS Birren.B., Linton.L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Bairen.B., Linton.L., Boukhgalter,B., Bournon,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Cammarata,J., Campoplano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karls,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C., H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Riback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Riley,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zalnoun,J., Zembek,L., Zinmer,A. and Zody,M.
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Homo sapiens chromosome 18, clone RP11-2E13, complete sequence
AC013759
                                                                                                                                                                                                                                                                                               Submitted (29-JUN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 13, 2001 this sequence version replaced gi:14017510. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                         Center project Information Center project name: L2525 Center clone name: 2_E_13
                                                                                                                                                   Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                   Center code: WIBR
                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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     Location/Qualifiers
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                                                                                                                                                                                                                                                   Center
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9735. .99
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849. .1317
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/rpt_family="L2"
complement(15368..15499)
                                                                                                   /rpt_t
18884.
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18760
                                                                                                                                                                                                                                            complement(15655.
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complement(14284..14469)
/rpt_family="MIR3"
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complement(10035. .1
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9412. .9466
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complement(5994..6)
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4827. .4985
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3471. .35
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complement/2210
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complement(2400
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/db_xref="taxon:9606"
     complement(19676. .19826)
                                                                                                                                                                                                                                                                                                                                                                                          complement(14465. .14556)
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complement(8462
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                                                                       family-"MLT1A2"
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Best Local Similarity 88.6%;
Matches 1148; Conservative
                                            42904 AGGGGAAGAATGCTGTTATTGTTAATCAATCCGGAATCATCACCGAGAAAGTT----A 42959
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           181 cctcagccaatggatgccctggactctccccttcttaggacctctagcagctataatatt 240
                                                                                                                               61 aggggaagaatgctgttagtatgttaatcaatctggaatcattactgagaaagttaaaga 120
                                                                                                                                                                                                1 tcbaaatcgaagagctttagacttgctaaccgccaaaagagggggaacctgtttattttt 60
                                                                                                                                                                                                                                                                                                                                                                                                   complement(32849...33446)
/rpt_family="Tigger3(Golem)"
complement(33448...33750)
/rpt_family="AluSg"
complement(33778...34403)
/rpt_family="PabL_B"
complement(34432...34481)
/rpt_family="PabL_B"
complement(34432...34531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(26203. .26366)
/rpt_family="MIR"
complement(26379). .26779)
/rpt_family="MSTB"
27372. .27438
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/rpt_family="AluSx"
complement(22028. .22245)
/rpt_family="LIMB8"
22383 .22658
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complement(1991. 20119)
/rpt_family="MIR"
complement(20181. 20673)
/rpt_family="MLT1G3"
                                                                                                                                                                                                                                                                                                           /rpt_fam1ly-"Tigger3(Golem)"
34740. .34928
/rpt_fam1ly-"MER58A"
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28669. .29257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="MLT1A1"
complement(23084. .23320)
/rpt_family="L1ME4A"
23541. .23586
                                                                                                                                                                                                                                                                                                                                                            complement(34482...34531)
/rpt_family="Tigger3(Golem)"
complement(34540...34639)
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/rpt_family="MER65A"
complement(30935...31258)
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complement(24127. .24226)
/rpt_family="MTR3"
24660. .24769
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29489. .29841
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ement(32840
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                                                                                                                                                                                                                                              Score 989.6; DB 9;
Pred. No. 4.9e-290;
0; Mismatches 117;
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	ccatttgggaagtggccactgccattttggtagc 1280	1246	Qy
44088	TCCATTCCTTGGAATCCATGAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTTGCCA	44029	ДD
1245	ttccattccttggtatctgtgaggccaagaaccccaggtcagagaangtgaggcttgcca	1186	γo
1185 44028	gttetettecatgacccaeggettetaatagagetataacacteaccgcatggeccaaga	1126 43969	D
1125 43968	gcatggctaagtgoctgggtttgtoctaatagaactgaacactggtcactgggttccatg	1066 43910	Qу
1065 43909	ctgatccagcgaggtacccattgccactcccgatcaggctaaaggcttgccattgttcct	1006 43850	dg VQ
1005 43849	cgtcacagacccgctgctgacttccatccctttggatccagcagagtgtccactgtgctc	946 43790	DB Qy
945 43789	tttttatgetcaagetgagettttgttegecatecaecaetgetgtttgeae	891 43730	Оу
890 43729	tetgtttteaetetattteaetetattaaateatgeaaetgeaetettetggteegtg 	833 43680	Db Qy
832 43679	ctcaggcattcaagccagcaacagcaacccctttgggtcccctcccattgtatgggagc	773 43620	P Qy
772 43619	caatagccaatcatctattgcctgagagcacagcgggaaggacaaggattgggatataaa	713 43560	Db Qy
712 43559	accatcagagagctcactaaaatgctaatcaggcaaaaacaggaggtaaag	661 43500	Db Qy
660 43499	anctgggaaggtgaccgcatccatctttaaacatggggcttgcaacttagctcacacccg	601 43440	Db Qy
600 43439	gggtggactgagagacaggactagctggatttcctaggctgactaagaatcccnaagcct	541 43380	Db Db
540 43379	aagcagttagagcagttgtcagccaacctccccaacagtacttgggttttcctgttgaga 	481 43320	Db Qy
480 43319	agtcacccctcccgaggaaatctcaactgcacaacccctactacactccaattcagtagg	421 43260	Db Qy
420 43259	aatctaccgtggacccctggaccggcctgctagactatgctctgatgttaatgacattga	361 43200	Db Qy
360 43199	tgaagctgtaaagctacaaatagttcttcaaatggaaccccagatgcagtccatgactaa 	301 43140	Qy dd
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44089 CCATTTTGGAAGTGGCCTGCTGCCATCTTGGGAGC 44123

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RESULT 10
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (17-Mar-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Only in DataBase (2000) In press 2 (bases 1 to 186911)
2 (bases 1 to 186911) Toyoda, A., Taylor, T. I
                                                                                                                                                                                                                                                                                                             preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Chemical Research (RIKEN), Genomic Sciences Center 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hattori, M., Ishii, K., Toyoda, A., Fujiyama, A., Yada, T., Totoki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hattori,M., Ishii,K., Toyoda,A., Fujiyama,A., Yada,T., Totoki,Y., Homo sapiens 186,911 genomic DNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The tradeer of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 9.41x in Q20 bases; sum-of-contigs
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147361: contig of 14725 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Only in DataBase (2000) In press 2 (bases 1 to 118241) Shimizu,N., Kudoh,J. and Shibuya,K. Direct Submission Submitted (04-APR-2000) to the DDBJ/EMBL/GenBank databases. Submitted (04-APR-2000) to the DDBJ/EMBL/GenBank databases. Nobuyoshi Shimizu, Keio University, School of Medicine, Moleo Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370,
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Shimizu,N., Kudoh,J. and Shibuya,K. Homo sapiens genomic DNA, chromosom
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Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
Ohki,M., Takagi,T., Sakaki,Y., Taudien,S., Blechschmidt,K.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R.,
Polley,A., Menzel,U., Delabar,J., Kumpf,K., Lehmann,R., Schudy,A.,
Patterson,D., Reichwald,K., Rump,A., Schillnabel,M., Schudy,A.,
Patterson,D., Rosenthal,A., Kudoh,J., Shbuya,K., Kawasaki,K.,
Asakawa,S., Shintani,A., Sasaki,T., Nagamine,K., Mitsuyama,S.,
Antonarakis,S.E., Minoshima,S., Shimzu,N., Nordslek,G.,
Hornischer,K., Barandt,P., Scharfe,M., Schoen,O., Desario,A.,
Reichelt,J., Kauer,G., Bloecker,H., Ramser,J., Beck,A., Klages,S.,
Hennig,S., Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K.,
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing Consortium: *RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses see below) on May 30, 2000 this sequence version replaced gi:7717295.

The chromosome 21 mapping and sequencing consortium consisting of * RIKEN Genomic Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan, * e.mail: hattoriggsc.riken.go.jp * URL: http://hgp.gsc.riken.go.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * Institute of Molecular Biotechnology, Genome Beutenbergstrasse 11, D-07745 Jena, Germany, e.mail: gscj-submit@genome.imb-jena.de
* e.mail: gscj-submit@genome.imb-jena.de
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Park,H.S., Toyoda,A., Ishii,K., Totoki,Y., Choi,D.K., Soeda,E.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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* e.mail: nshimizu@dmb-med.keio.ac.
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Inhestrasse 73, D-14195 Berlin, (
Inhestrasse 73, D-14195 Berlin, (
e e mail: info-chr21@molgen.mpg.de
URL: http://chr21.rz-berlin.mpg.c
L163242: Submitted (10-Apr-2000).
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Score 985.6; DB 9;
Pred. No. 8.1e-289;
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Best Local Similarity 88.1
Matches 1119; Conservative
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AP001600.1
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 91097)
Shimizu,N., Kudoh,J. and Shibuya,K.
Homo sapiens genomic DNA, chromosome 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Only in DataBase (2000) In (2005) 2 (Dass 1 to 91097) Shimizu,N., Kudoh,J. and Shibuya,K. Direct Submission
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/clone_lib="Keio
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1. .91097
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Pred. No. 2.4e-288;
0; Mismatches 123;
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                                              AUTHORS
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Homo sapiens chromosome 12 clone
SEQUENCE, 20 unordered pieces.
AC008121
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 172721)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
                                                                                                           Homo sapiens
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Bryant, N.P.,
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JOURNAL REFERENCE

TITLE

AUTHORS TITLE

JOURNAL

COMMENT

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 20 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will

NOTE: Estimated insert size may differ from sequence length

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Burch, P., Burkett, C., Burcell, K.L., Byrd, N.C., Carron, T., Carren, T., Carren, T., Chen, G., Chen, G., Chen, G., Chen, E., Carren, T., Chen, G., Chen, G., Chen, E., Chen, Z., Chowshry, I., Christopoulos, C., Cleveland, C.D., Cox.C., Coyle, M.D., Dabborne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dabborne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dabborne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, I., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K., Barls, T., Ferraguic, D., Plagy, N., Ford, T., Fell, S., Ferraguic, D., Plagy, N., Ford, T., Fell, S., Ferraguic, D., Plagy, N., Ford, T., Ferraguic, D., Ford, N., Ford, T., Ferraguic, D., Ford, N., Ford, N., Ferraguic, D., Ford, N., Ford, N., Ferraguic, D., Ford, N., Ferraguic, D., Ford, N., Ferraguic, D., Ford, N., Ferraguic, T., Ferraguic, D., Ford, N., Ferraguic, N., Ford, N., Ford, N., Ferraguic, N., Ford, N., Ford
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Best Local Similarity 86.5%;
Matches 1158; Conservative
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/clone="RP11-407N8"
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303: contig o
403: gap of u
403: gap of u
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463: gap of u
563: gap of u
284: gap of u
284: gap of u
285: gap of u
601: contig o
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Pred. No. 6.6e-288;
0; Mismatches 157;
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y of 5207 bp in length
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	1312 aaggatcccccagtaaca 1329 	Оу
1311 40005	1252 gggaagtggccactgccattttggtagcggcccaccaccatcttgggagctgtggggagctgtgggagctgtgtgggagctgtgtgggagctgtgggagctgtgggagctgtgggagctgtgggagctgtgggagctgtgggagctgtggaagctgtggaagctgtggaagctgtggaagctgtggaagctgggaagctgggaagctgggaagct	Qy Db
1251 39946	1192 tccttggtatctgtgaggccaagaaccccaggtcagagaangtgaggcttgccaccattt	Ор
1191 39887	1132 ttccatgacccacggcttctaatagagctataacactcaccgcatggcccaagattccat	Qy db
1131 39827	1072 ctaagtdcctgggtttgtcctaatagaactgaacactggtcactgggttccatggttctc	Оу
1071 39767	1012 cagcgaggtacccattgccactcccgatcaggctaaaggcttgccattgttcctgcatgg	Qy Db
1011 39707	952 agaccegetgetgacttccatecetttggatecageagagtgtccactgtgetectgate	Db dg
951 39647	892 ttttatggctcaagctgagcttttgttcgccatccaccactgctgttttgccaccgtcac	pb dy
891 39587	832 ototyttttoactotatttoactotattaaatcatgoaactgoactottotggtocgtgt	Db Qy
831 39539	773 ctcaggcattcaagccagcaacagc-aaccccctttgggtcccctcccattgtatgggag 	Db Qy
772 39479	713 caatagccaatcatctattgcctgagagcacagcgggaaggacaaggattgggatataaa 	Db Qy
712 39419	661 accaatcagagagctcactaaaatgctaatcaggcaaaaacaggaggtaaag	ОУ
660 39359	601 anctgggaaggtgaccgcatccatctttaaacatggggcttgcaacttagctcacacccg 	ОУ
600 39299	541 gggtggactgagagacaggactagctggatttcctaggctgactaagaatcccnaagcct	pb dy
540 39239	481 aagcagttagagcagttgtcagccaacctccccaacagtacttgggttttcctgttgaga 	ОУ
480 39179	421 agtcaccctcccgaggaaatctcaactgcacaacccctactacactccaattcagtagg	Qy Db
420 39119	361 aatctaccgtggacccctggaccggcctgctagactatgctctgatgttaatgacattga	Оу
360 39059	301 tgaagctgtaaagctacaaatagttcttcaaatggaaccccagatgcagtccatgactaa 	Qy Db

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 27, 2000 this sequence version replaced gi:6466621. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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1 (bases 1 to 145785)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 136152 bases at least Q40
Consensus quality: 140073 bases at least Q30
Consensus quality: 141078 bases at least Q20
Insert size: 187000; agarose-fp
Insert size: 144185; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project Information Center project name: L3813 Center clone name: 440_C_21
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Center: Whitehead Institute/ MIT Center for Genome Research
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100 bp 2628: contig of 1197 bp in length 2629 2728: gap of 100 bp 3745: contig of 7546 3846
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sum-of-contigs
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* 62674 62773; gap of 100 bp 11

* 62774 75359; contig of 12586 bp 11

* 75360 75459; gap of 100 bp 100

* 75460 90704; contig of 15245 bp in 100 bp 100 
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6428 7950: contig of 100 bp
6528 8050: gap of 100 bp
10578: contig of 2528 bp in 1
10579 10678: gap of 100 bp
10679 15308: contig of 4630 bp in 1k
15309 15408: gap of 100 bp
15409: 20910: contig of 5502 bp in ler.
20911 21010: gap of 100 bp
20910: contig of 5502 bp in ler.
20911 25032: contig of 4022 bp in ler.
20913 25132: gap of 100 bp
2130 25132: contig of 3997 bp in lengt
2130 2929: gap of 100 bp
2130 29529: gap of 100 bp
2130 36550: contig of 7321 bp in length
2130 48963: contig of 12313 bp in length
2130 48963: contig of 12313 bp in length
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Db	6951	6951 CAGACCCGTGGCTGACTTCCATCCCTCCAGATCTGGCAGGGTGTCCACTGTGCTCCTGAT 6892	
Qy	1011	ccagcgaggtacccattgccactcccgatcaggctaaaggcttgccattgttcctgcatg 1070	
DЬ	6891	CCAGCGAGGCACCCATTGCCGCTCCCAATCGGGCTAAAGCCTTGCCATTGTTCCTGCACA 6832	
Qy	1071	gctaagtgcctgggtttgtcctaatagaactgaacactggtcactgggttccatggttct 1130	
Ъ	6831	6831 GCTAAGTGCCTGGGTTCGTCCTAATCAAGCTGAACACTAGTCACTGGGTTCCATGGTTCT 6772	
Qy	1131	1131 cttccatgacccacggcttctaatagagctataacactcaccgcatggcccaagattcca 1190	
Db	6771	6771 CTTCCATGACCCATGGCTTCTAATAGAGCTATAACACTCACCGCATGGCCCAAGATTCCA 6712	
Qy	1191	ttccttggtatctgtgaggccaagaaccccaggtcagagaangtgaggcttgccaccatt 1250	
DЪ	6711	TTCCTTGGAATCCGTGAGGCCAAGAACCCCAGGTCAGAGAACACGAGGCTGCCTGC	
Qy	1251	1251 tggga 1255	
망	6651	6651 TGGAA 6647	

Search completed: June 20, 2002, 10:15:40 Job time: 12665 sec

OLASON AMALIA JEWA SHITA